

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:49:23 ; Search time 46 Seconds
(without alignments)
1897.373 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTSPSSSTALASCRIARR.....SQAQTLLDSVYSHLPDLL 655

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_101002.*

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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	100.0	655	20 AAY41693	Human PRO868 prote
2	655	100.0	655	20 AAW81059	Novel human tumor
3	655	100.0	655	21 AAB26981	Human tumor necro
4	655	100.0	655	21 AAB01349	Tumour necrosis fa
5	655	100.0	655	21 AAB01338	DR-6 death recepto
6	655	100.0	655	21 AAY77460	Human TNF receptor
7	655	100.0	655	22 AAU29232	Human PRO polypt
8	655	100.0	655	23 AAE21958	Human death domain
9	655	100.0	691	21 AAY92846	Human osteoprotegr
10	631	96.3	631	20 AAY05678	Human full-length

11	631	96.3	631	23 AAE21959	Human death domain
12	631	96.3	655	19 AAW75792	Human tumour necro
13	554	84.6	655	21 AAB44249	Human PRO868 (UNO4
14	544	83.1	605	20 AAY05697	Human TNF receptor
15	541	82.6	655	22 AAB93023	Human protein sequ
16	479	73.1	508	20 AAY05680	Tumour necrosis fa
17	415	63.4	444	21 AAY77461	Human TNF receptor
18	405	61.8	405	21 AAY67947	Human DETH protein
19	326	49.8	393	20 AAY28450	A human tumour nec
20	250	38.2	254	21 AAY92843	Human osteoprotegr
21	249	38.0	253	20 AAY05696	Human TNF receptor
22	225	34.4	229	20 AAY05679	Human soluble tumo
23	218	33.3	222	22 AAM56603	Human brain expres
24	218	33.3	222	22 AAM16812	Peptide #3246 enco
25	218	33.3	222	22 AAM29294	Peptide #3331 enco
26	218	33.3	222	22 AAM04528	Peptide #3210 enco
27	218	33.3	222	23 ABG38570	Human peptide enco
28	184	28.1	290	21 AAY92842	Human osteoprotegr
29	184	28.1	290	21 AAY92844	Human osteoprotegr
30	164	25.0	164	21 AAB00012	Peptide fragment o
31	125	19.1	125	19 AAW75793	Tumour necrosis fa
32	119	18.2	147	21 AAB26985	Human TNF receptor
33	116	17.7	573	20 AAY05695	Mouse TNF receptor
34	116	17.7	600	21 AAY92845	Murine osteoprotegr
35	86	13.1	210	21 AAY77459	Human TNF receptor
36	85	13.0	85	22 ABB29318	Peptide #1969 enco
37	85	13.0	85	22 ABB30755	Peptide #3406 enco
38	85	13.0	85	22 ABB35932	Peptide #3438 enco
39	85	13.0	85	22 ABB19901	Protein #1900 enco
40	85	13.0	85	22 ABB21341	Protein #3340 enco
41	85	13.0	85	22 AAM55278	Human brain expres
42	85	13.0	85	22 AAM56735	Human brain expres
43	85	13.0	85	22 AAM67675	Human bone marrow
44	85	13.0	85	22 AAM69113	Human bone marrow
45	85	13.0	85	22 AAM15484	Peptide #1918 enco

ALIGNMENTS

RESULT 1

AAAY41693
ID AAY41693 standard; Protein; 655 AA.

XX AC AAY41693;

XX DT 07-DEC-1999 (first entry)

XX DE Human PRO868 protein sequence.

XX KW Human; PRO; EST: expressed sequence tag; PCR primer; hybridisation;
XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX KW secreted protein; transmembrane protein.

XX OS Homo sapiens.

XX PN WO9946281-A2.

XX PD 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1998; 98US-0077450.

XX PR 11-MAR-1998; 98US-0077632.

XX PR 11-MAR-1998; 98US-0077641.

XX PR 11-MAR-1998; 98US-0077649.

XX PR 12-MAR-1998; 98US-0077791.

XX PR 13-MAR-1998; 98US-0078004.

XX PR 17-MAR-1998; 98US-0040220.

XX PR 20-MAR-1998; 98US-0078886.

XX PR 20-MAR-1998; 98US-0078910.

XX PR 20-MAR-1998; 98US-0078936.

XX PR 20-MAR-1998; 98US-0078939.

PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 29-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 13-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 15-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085373.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 26-MAY-1998; 98US-0087098.

PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 XX WPI; 1999-551358/46.
 DR N-PSDB; AA233945.
 DR
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 XX
 XX
 PS Claim 12; Fig 26; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA233891 to
 CC AA234338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 655 AA;
 Query Match 100.0%; Score 655; DB 20; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFLSTTTAAQPEQKASNLICTYRHVDRA 60
 DB 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFLSTTTAAQPEQKASNLICTYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTTRHENGIEKCHDCSQPCPWPMEK 120
 DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTTRHENGIEKCHDCSQPCPWPMEK 120
 QY 121 LPCAALTDRCTCPGCMFQSNATCAPHTVCPGVGWYKKGTTEDVRCQKARGTSDVP 180
 DB 121 LPCAALTDRCTCPGCMFQSNATCAPHTVCPGVGWYKKGTTEDVRCQKARGTSDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFRPEHMETHE 240
 DB 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSSASVPRPKVLSIQEGTVPDNTSSARGKEDVNTLPNLOVNH 300
 DB 241 VPSSTYVPKGMNSTESNSSASVPRPKVLSIQEGTVPDNTSSARGKEDVNTLPNLOVNH 300
 QY 301 QOQPHRHILKLLPSMEATGGEKSSPTPIKGRGHPRQNLHKHFDINEHLPWIVLFLLL 360
 DB 301 QOQPHRHILKLLPSMEATGGEKSSPTPIKGRGHPRQNLHKHFDINEHLPWIVLFLLL 360
 QY 361 VLWVIIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTTONREKWIYCNHGHDILK 420
 DB 361 VLWVIIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTTONREKWIYCNHGHDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTAADHERAYAAALQHTTIRGPASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTAADHERAYAAALQHTTIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLSPSPSPSPSPSPSPSPSPSPSPSPSP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPSPLSPSPSPSPSPSPSPSPSPSPSPSPSP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSSSALSRSNGSFITKEKDDTVLRQVRLDPCDLPITF 600

|||||
541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKDVLVLRQVRLDPCDLQPIF 600
QY 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASOTLLDSVYSHLPDLL 655
|||||
Db 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASOTLLDSVYSHLPDLL 655

RESULT 2

AAW81059

ID AAW81059 standard; Protein: 655 AA.

XX AC AAW81059;

DT 10-MAY-1999 (first entry)

DE Novel human tumor necrosis factor receptor TR9.

XX Human; tumour necrosis factor receptor; TNFR; TR9 receptor; cancer;
KW apoptosis; agonist; inhibition; autoimmune disorder; viral infection;
KW inflammation; antagonist; AIDS; neurodegenerative disorder.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..40

FT Peptide /note= "signal peptide"

FT Peptide 41..655

FT Peptide /note= "mature protein"

XX W09856892-A1.

PN 17-DEC-1998.

XX 10-JUN-1998; 98WO-US11932.

XX 11-JUN-1997; 97US-0052991.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fan P, Gentz RL, Ni J, Yu G;

XX WPI; 1999-060325/05.

DR N-PSDB; AAW99927.

XX New isolated tumour necrosis factor-like receptor, TR9 - used to
PT develop products for treating e.g. cancers, autoimmune disorders,
PT viral infections, inflammation, graft rejection, neurodegenerative
PT disorders or ischaemic injury

XX Claim 1; Fig 1; 134pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor
CC receptor (TNFR), TR9 receptor, used in the method of the invention
CC to develop products to treat disorders such as cancers. The novel
CC TNFR, TR9, can be used to identify agents for modifying apoptosis.
CC Agonists can be used to treat diseases associated with increased
CC cell survival, or the inhibition of apoptosis, including cancers
CC (e.g. follicular lymphomas, carcinomas with p53 mutations, and
CC hormone-dependent tumours, such as breast cancer, prostate cancer,
CC Kaposi's sarcoma and ovarian cancer), autoimmune disorders (e.g.
CC systemic lupus erythematosus and immune-related glomerulonephritis
CC rheumatoid arthritis), viral infections (e.g. herpes viruses, pox
CC viruses and adenoviruses), inflammation, graft vs host disease,
CC acute graft rejection and chronic graft rejection. Antagonists
CC can be used to treat diseases associated with increased apoptosis
CC including AIDS, neurodegenerative disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC retinitis pigmentosa, cerebellar degeneration), myelodysplastic
CC syndromes (e.g. aplastic anemia), ischemic injury (e.g. that
CC caused by myocardial infarction, stroke and reperfusion injury),
CC toxin-induced liver disease (e.g. that caused by alcohol), septic
CC shock, cachexia, anorexia, inflammatory diseases and stress responseCC related diseases, such as inflammatory bowel disease, rheumatoid
CC arthritis, osteoarthritis, psoriasis and septicemia. The products
CC can also be used for detection and diagnosis.

SQ Sequence 655 AA;

Query Match 100.0%; Score 655; DB 20; Length 655;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTVRHVDRA 60

Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTVRHVDRA 60

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Db 61 TGOVLTCDCPKAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKDCSCPCPWPMEK 120

QY 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTETEDVRCQKARGTFSDVP 180

Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTETEDVRCQKARGTFSDVP 180

QY 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSSSSTSPSGTAIFRPRHEMTH 240

Db 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSSSSTSPSGTAIFRPRHEMTH 240

QY 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARGKEDVNTKLPNLQVNH 300

Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARGKEDVNTKLPNLQVNH 300

QY 301 QQGPVHRRHILKLLPSMEATGGEKSTPIKGPGRHPRQNLKHFDINHLPMIVLFLLL 360

Db 301 QQGPVHRRHILKLLPSMEATGGEKSTPIKGPGRHPRQNLKHFDINHLPMIVLFLLL 360

QY 361 VLVVIVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNKREKIYYCNGHGIDLK 420

Db 361 VLVVIVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNKREKIYYCNGHGIDLK 420

QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTAADHERAYAAALQHWITRGPEASLAQLIS 480

Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSNGYTAADHERAYAAALQHWITRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETKLALPMSPLSPSPISPNKLENSALLTVPEP 540

Db 481 ALRQHRNDVVEKIRGLMEDTTQLETKLALPMSPLSPSPISPNKLENSALLTVPEP 540

QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKDVLVLRQVRLDPCDLQPIF 600

Db 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKDVLVLRQVRLDPCDLQPIF 600

QY 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASOTLLDSVYSHLPDLL 655

Db 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASOTLLDSVYSHLPDLL 655

RESULT 3

AAB26981

ID AAB26981 standard; Protein: 655 AA.

XX AAB26981;

AC AAB26981;

DT 02-FEB-2001 (first entry)

XX Human tumour necrosis factor receptor TR9.

XX Human; tumour necrosis factor; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;

CC length gene may be used as hybridization probes for a cDNA library to
CC isolate the full length gene and to isolate other genes which have a
CC high sequence similarity. The probes may be used to identify a cDNA
CC clone corresponding to a full length transcript and a genomic clone
CC or clones that contain the complete gene including regulatory and
CC promoter regions, exons, and introns.

xx SQ Sequence 655 AA;
Query Match 100.0%; Score 655; DB 21; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLGLFLSTTTAAQPEKASNLIGTYRHVDRA 60
Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLGLFLSTTTAAQPEKASNLIGTYRHVDRA 60
Qy 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEK 120
Db 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEK 120
Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
Qy 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPSPSSSTSPSGTAIPRPEHMETHE 240
Db 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPSPSSSTSPSGTAIPRPEHMETHE 240
Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Qy 301 QOGPHRHILKLLPSMEATGKESSTPIKPKRGHPRONLKHKHPDINEHLPMWIVLFLLL 360
Db 301 QOGPHRHILKLLPSMEATGKESSTPIKPKRGHPRONLKHKHPDINEHLPMWIVLFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSWTPTQNRKWIYCNHGIDILK 420
Db 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSWTPTQNRKWIYCNHGIDILK 420
Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWIRGPEASLAQLIS 480
Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWIRGPEASLAQLIS 480
Qy 481 ALRQHRNDVVVEKIRGLMEDTQLETDLKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Db 481 ALRQHRNDVVVEKIRGLMEDTQLETDLKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Qy 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSSALSRSNGSFITKEKDTVLRQVRLDPCDLQPIF 600
Db 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSSALSRSNGSFITKEKDTVLRQVRLDPCDLQPIF 600
Qy 601 DMLHFLNPELRVIEIPOAEDKLDRLFEIIGVKSQEASQTLSDSYSHLPDLL 655
Db 601 DMLHFLNPELRVIEIPOAEDKLDRLFEIIGVKSQEASQTLSDSYSHLPDLL 655

RESULT 5

AAB01338
ID AAB01338 standard; Protein: 655 AA.
xx AC AAB01338;
xx DT 25-SEP-2000 (first entry)
xx XX
DE DR-6 death receptor.
xx UL144; death receptor; apoptosis; programmed cell death; Fas;
xx TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
xx human.
xx OS Homo sapiens.

xx WO2000034335-A2.
xx 15-JUN-2000.
xx 03-DEC-1999; 99WO-US26035.
xx 04-DEC-1998; 98US-0205018.
xx (SCHE) SCHERING CORP.
xx PI Leong C, Phillips JH;
xx WPI; 2000-423383/36.
xx Purified or recombinant polypeptide for modulating apoptosis comprises
xx a sequence which binds to an antibody specific for ULL144 or its
xx fragments
xx Disclosure; Page 68-70; 76pp; English.
xx A pure or recombinant polypeptide which binds to a polyclonal antibody
xx specific for the mature Ull144 is useful for screening molecules which
xx block induction of apoptosis or interfere with antiapoptotic activity.
xx The polypeptide is also useful for modulating apoptosis and useful in
xx treatment of conditions associated with abnormal physiology or
xx development, such as cancer or degenerative conditions and for
xx regulation of viral infection and replication. At least five
xx different death receptors are known, which include the CD95
xx (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
xx protein (TRAMP), death receptor-6 (DR-6), and TNF-related
xx apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
xx SQ Sequence 655 AA;
Query Match 100.0%; Score 655; DB 21; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLGLFLSTTTAAQPEKASNLIGTYRHVDRA 60
Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLGLFLSTTTAAQPEKASNLIGTYRHVDRA 60
Qy 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEK 120
Db 61 TGOVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEK 120
Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVKRGKGTETEDVRCKOCARFTSDVP 180
Qy 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPSPSSSTSPSGTAIPRPEHMETHE 240
Db 181 SSVMKCKAYTDCLSONLVWIKPGTKETDNVCGTLPSPSSSTSPSGTAIPRPEHMETHE 240
Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
Qy 301 QOGPHRHILKLLPSMEATGKESSTPIKPKRGHPRONLKHKHPDINEHLPMWIVLFLLL 360
Db 301 QOGPHRHILKLLPSMEATGKESSTPIKPKRGHPRONLKHKHPDINEHLPMWIVLFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSWTPTQNRKWIYCNHGIDILK 420
Db 361 VLVVIVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSWTPTQNRKWIYCNHGIDILK 420
Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWIRGPEASLAQLIS 480
Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWIRGPEASLAQLIS 480
Qy 481 ALRQHRNDVVVEKIRGLMEDTQLETDLKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Db 481 ALRQHRNDVVVEKIRGLMEDTQLETDLKALPMSPLSPSPIPSPNAKLENSALLTVEP 540

Db 481 ALRQHRNDVVEKIRGLMEDTTOLETDKLALPMSPLSPSPSPNAKLNSALLTVEP 540
 QY 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITREKKTDLVLRQVRLDPCDLOPIF 600
 Db 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITREKKTDLVLRQVRLDPCDLOPIF 600
 QY 601 DDLHLFNLPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
 Db 601 DDLHLFNLPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655

RESULT 6
 AAY77460
 ID AAY77460 standard; Protein: 655 AA.
 AC AAY77460;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Human TNF receptor-like protein HSLJD37R, SEQ ID NO:10.
 XX
 KW TNF receptor family; tumour necrosis factor: HDTEA84; HSLJD37R;
 KW Rank-like protein; RANKL; immune disorder; inflammation; allergy;
 KW immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory;
 KW dermatological; antithyroid.
 XX
 OS Homo sapiens.
 XX
 XX W0200001817-A2.
 PN
 XX 13-JAN-2000.
 PD
 XX
 XX 06-JUL-1999; 99WO-US12366.
 XX
 PR 06-JUL-1998; 98US-0110938.
 PR 13-JUL-1998; 98US-0114466.
 PR 23-JUL-1998; 98US-0093897.
 PR 12-AUG-1998; 98US-0132968.
 PR 18-AUG-1998; 98US-0136214.
 PR 11-SEP-1998; 98US-0099999.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 XX Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
 PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
 PI Bazan JF, Mahony D, Lees EM;
 XX
 XX WPI: 2000-171015/15.
 DR N-PSDB; AA292406.
 DR
 XX
 PT New isolated mammalian genes, used to develop products for treating
 PT e.g. immune, inflammatory or allergic abnormalities, cancers or
 PT degenerative conditions
 XX
 PS Claim 24; Page 163-165; 218pp; English.

The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL; human CC chemokine HCC5; human deubiquitinating proteins DUB1 and DUB12; human MD-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proliferation, or differentiation of cells), or are intracellular proteins which are important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or allergic disorders, or abnormal cellular proliferation, for example,

CC cancers or degenerative conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's thyroiditis, as well as acute and chronic inflammatory responses in which T cell activation, expansion, and/or immunological T cell memory play an important role. Sequences AAY77458-Y77461 and AAY77465-Y77468 represent TNF receptor family-related proteins. AAY77458 is the human protein HDTEA84, AAY77459-Y77461 are human HSLJD37R proteins, AAY77465 is murine Rank-like protein RANKL, and AAY77466-Y77468 are human RANKL proteins.

XX
 SQ Sequence 655 AA;
 Query Match 100.0%; Score 655; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels. 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAAQPEQKASNLIGTYRHVDRA 60
 Db 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNLSRVCSGPCVGTETRHENGIEKCHDCSQCPWPMIEK 120
 Db 61 TGOVLTCDCPCAGTYVSEHCTNLSRVCSGPCVGTETRHENGIEKCHDCSQCPWPMIEK 120
 QY 121 LPCAALTDRRECTCPGCMFQSNATCAPHTVCPVGWGVKKGKGTETEDYRCQKARGTSDVP 180
 Db 121 LPCAALTDRRECTCPGCMFQSNATCAPHTVCPVGWGVKKGKGTETEDYRCQKARGTSDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 Db 181 SSVMKCKAYTDCLSQNLVVKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPGKMNSTESNSSASVPRPKVLSSTOECTVDPNTSSARGKEDVANKTLPNLQVNH 300
 Db 241 VPSSTYVPGKMNSTESNSSASVPRPKVLSSTOECTVDPNTSSARGKEDVANKTLPNLQVNH 300
 QY 301 QQGPHRHRLKLLPSMEATGGKSSSTPIKPKRGHPRQNLHKHFDINEHLPWMIVLFLLL 360
 Db 301 QQGPHRHRLKLLPSMEATGGKSSSTPIKPKRGHPRQNLHKHFDINEHLPWMIVLFLLL 360
 QY 361 VLVVIVVCSIRKSRRLKKGPRQDPSAIVEKAGLKKKSMPTONREKWIYVNGHGDILK 420
 Db 361 VLVVIVVCSIRKSRRLKKGPRQDPSAIVEKAGLKKKSMPTONREKWIYVNGHGDILK 420
 QY 421 LVAAQVGSOWKDIYQFLCNASREVAAFNGYTAADHERAYAAALQHWITIRGPEASLAQLIS 480
 Db 421 LVAAQVGSOWKDIYQFLCNASREVAAFNGYTAADHERAYAAALQHWITIRGPEASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTOLETDKLALPMSPLSPSPSPNAKLNSALLTVEP 540
 Db 481 ALRQHRNDVVEKIRGLMEDTTOLETDKLALPMSPLSPSPSPNAKLNSALLTVEP 540
 QY 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITREKKTDLVLRQVRLDPCDLOPIF 600
 Db 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRLNGSFITREKKTDLVLRQVRLDPCDLOPIF 600
 QY 601 DDLHLFNLPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
 Db 601 DDLHLFNLPELRLVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655

RESULT 7
 AAU29232
 ID AAU29232 standard; Protein: 655 AA.
 XX
 AC AAU29232;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #209.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

XX 03-MAR-2000; 2000US-187202P.

XX 06-MAR-2000; 2000US-186968P.

XX 14-MAR-2000; 2000US-189320P.

XX 14-MAR-2000; 2000US-189328P.

XX 15-MAR-2000; 2000WO-US06884.

XX 21-MAR-2000; 2000US-190828P.

XX 21-MAR-2000; 2000US-191007P.

XX 21-MAR-2000; 2000US-191048P.

XX 21-MAR-2000; 2000US-191314P.

XX 28-MAR-2000; 2000US-192655P.

XX 29-MAR-2000; 2000US-193032P.

XX 29-MAR-2000; 2000US-193053P.

XX 30-MAR-2000; 2000WO-US08439.

XX 04-APR-2000; 2000US-194449P.

XX 04-APR-2000; 2000US-194647P.

XX 11-APR-2000; 2000US-195975P.

XX 11-APR-2000; 2000US-196000P.

XX 11-APR-2000; 2000US-196187P.

XX 11-APR-2000; 2000US-196690P.

XX 11-APR-2000; 2000US-196820P.

XX 18-APR-2000; 2000US-198121P.

XX 18-APR-2000; 2000US-198585P.

XX 25-APR-2000; 2000US-199397P.

XX 25-APR-2000; 2000US-199550P.

XX 25-APR-2000; 2000US-199654P.

XX 03-MAY-2000; 2000US-201516P.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-2000; 2000WO-US15264.

XX 05-JUN-2000; 2000US-209832P.

XX 28-JUL-2000; 2000WO-US20710.

XX 22-AUG-2000; 2000US-0644848.

XX 24-AUG-2000; 2000WO-US23328.

XX 08-NOV-2000; 2000WO-US30952.

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and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 655 AA;

Query Match 100.0%; Score 655; DB 22; Length 655;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPKASNLGTYRHVDRA 60

DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPKASNLGTYRHVDRA 60

QY 61 TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCSPCPWPMTEK 120

DB 61 TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFTRHENGIEKCHDCSPCPWPMTEK 120

QY 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVGRKKGTTETEDVRCQKARGTFSVDP 180

DB 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGVGRKKGTTETEDVRCQKARGTFSVDP 180

QY 181 SSVMKCRAYTCLSONLVVVKPGTETDNVCGTLPSSSSSTSPSGTAIFRPRHEMETH 240

DB 181 SSVMKCRAYTCLSONLVVVKPGTETDNVCGTLPSSSSSTSPSGTAIFRPRHEMETH 240

QY 241 VPSSTYVPGKMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARKEDVNTKLPNQQVNH 300

DB 241 VPSSTYVPGKMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARKEDVNTKLPNQQVNH 300

QY 301 QGPHHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHHFDINEHLPMMIVLFLLL 360

DB 301 QGPHHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHHFDINEHLPMMIVLFLLL 360

QY 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWTYYCNGHIDILK 420

DB 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWTYYCNGHIDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAPSNCTADHERAYAAALQHWITRGPEASLAQLIS 480

DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAPSNCTADHERAYAAALQHWITRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540

DB 481 ALRQHRNDVVEKIRGLMEDTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540

QY 541 SPQDKNKGFFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTVLROVRDPCDLP 600

DB 541 SPQDKNKGFFVDESEPLLRCDSTSGSSALSRSNGSFITKEKKDVTVLROVRDPCDLP 600

QY 601 DDLHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKVQSEASQTLDSVSHLPDLL 655

DB 601 DDLHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKVQSEASQTLDSVSHLPDLL 655

RESULT 8

AAE21958

ID AAE21958 standard; Protein; 655 AA.

XX AC AAE21958;

XX XX 25-JUL-2002 (first entry)

XX DE Human death domain containing receptor (DR6) protein.

XX KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;

XX KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

XX 03-MAR-2000; 2000US-187202P.

XX 06-MAR-2000; 2000US-186968P.

XX 14-MAR-2000; 2000US-189320P.

XX 14-MAR-2000; 2000US-189328P.

XX 15-MAR-2000; 2000WO-US06884.

XX 21-MAR-2000; 2000US-190828P.

XX 21-MAR-2000; 2000US-191007P.

XX 21-MAR-2000; 2000US-191048P.

XX 21-MAR-2000; 2000US-191314P.

XX 28-MAR-2000; 2000US-192655P.

XX 29-MAR-2000; 2000US-193032P.

XX 29-MAR-2000; 2000US-193053P.

XX 30-MAR-2000; 2000WO-US08439.

XX 04-APR-2000; 2000US-194449P.

XX 04-APR-2000; 2000US-194647P.

XX 11-APR-2000; 2000US-195975P.

XX 11-APR-2000; 2000US-196000P.

XX 11-APR-2000; 2000US-196187P.

XX 11-APR-2000; 2000US-196690P.

XX 11-APR-2000; 2000US-196820P.

XX 18-APR-2000; 2000US-198121P.

XX 18-APR-2000; 2000US-198585P.

XX 25-APR-2000; 2000US-199397P.

XX 25-APR-2000; 2000US-199550P.

XX 25-APR-2000; 2000US-199654P.

XX 03-MAY-2000; 2000US-201516P.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-2000; 2000WO-US15264.

XX 05-JUN-2000; 2000US-209832P.

XX 28-JUL-2000; 2000WO-US20710.

XX 22-AUG-2000; 2000US-0644848.

XX 24-AUG-2000; 2000WO-US23328.

XX 08-NOV-2000; 2000WO-US30952.

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

XX 03-MAR-2000; 2000US-187202P.

XX 06-MAR-2000; 2000US-186968P.

XX 14-MAR-2000; 2000US-189320P.

XX 14-MAR-2000; 2000US-189328P.

XX 15-MAR-2000; 2000WO-US06884.

XX 21-MAR-2000; 2000US-190828P.

XX 21-MAR-2000; 2000US-191007P.

XX 21-MAR-2000; 2000US-191048P.

XX 21-MAR-2000; 2000US-191314P.

XX 28-MAR-2000; 2000US-192655P.

XX 29-MAR-2000; 2000US-193032P.

XX 29-MAR-2000; 2000US-193053P.

XX 30-MAR-2000; 2000WO-US08439.

XX 04-APR-2000; 2000US-194449P.

XX 04-APR-2000; 2000US-194647P.

XX 11-APR-2000; 2000US-195975P.

XX 11-APR-2000; 2000US-196000P.

XX 11-APR-2000; 2000US-196187P.

XX 11-APR-2000; 2000US-196690P.

XX 11-APR-2000; 2000US-196820P.

XX 18-APR-2000; 2000US-198121P.

XX 18-APR-2000; 2000US-198585P.

XX 25-APR-2000; 2000US-199397P.

XX 25-APR-2000; 2000US-199550P.

XX 25-APR-2000; 2000US-199654P.

XX 03-MAY-2000; 2000US-201516P.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-2000; 2000WO-US15264.

KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
 KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
 KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
 KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;
 KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
 KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
 KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
 KW dermatological; hepatotropic; antibacterial.

OS Homo sapiens.

PH Key Location/Qualifiers
 FT Peptide 1..41
 FT /label= Signal_peptide
 FT Protein 41..655
 FT /note= "Mature human DR6"
 FT Domain 39..76
 FT /note= "TNFR cysteine rich domain"
 FT Domain 77..118
 FT /note= "TNFR cysteine rich domain"
 FT Domain 119..162
 FT /note= "TNFR cysteine rich domain"
 FT Domain 163..201
 FT /note= "TNFR cysteine rich domain"
 FT Domain 339..351
 FT /note= "Transmembrane domain"
 FT Domain 360..370
 FT /note= "Transmembrane domain"

WO200185209-A2.

15-NOV-2001.

30-APR-2001; 2001WO-US11735.

10-MAY-2000; 2000US-203015P.

(ELIL) LILLY & CO ELI.

Heuer JG, Liu J, Na S, Song HY, Yang D;

WPI: 2002-351283/38.

N-PSDB; AAD35053.

Treating or preventing T cell or Th2 cell mediated condition e.g.,
 asthma or multiple sclerosis in mammal, comprises administering
 composition comprising death domain containing receptor, DR6 agonist or
 antagonist -

Claim 11; Page 126-129; 133pp; English.

The invention relates to a method for treating or preventing a T cell
 mediated condition or a Th2 cell mediated condition in a mammal. The
 method comprising administering to the mammal a pharmaceutical
 composition comprising a death domain containing receptor (DR6) agonist
 or antagonist. The method is useful for treating or preventing a T cell
 mediated condition or a Th2 cell mediated condition in a mammal. A DR6
 agonist is useful in the manufacture of a medicament for treating or
 preventing at least one symptom associated with aberrant apoptosis.
 A DR6 antagonist is useful in the manufacture of a medicament for
 preventing at least one symptom associated with aberrant apoptosis.
 graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma,
 atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
 insulin-dependent diabetes mellitus, cancer, multiple sclerosis,
 Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic
 lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
 autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
 lung disease, organ rejection after transplantation, thrombotic
 thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
 uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
 dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
 or a condition or symptom related to the above mentioned diseases in a
 mammal. An DR6 antagonist is useful in the manufacture of a medicament
 for treating or preventing at least one symptom associated with
 immunodeficiency, aberrant apoptosis, bacterial, viral or microbial

CC infection, complications of infection, human immunodeficiency virus
 CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
 CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
 CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
 CC associated ulceration, cytoprotection during cancer treatment,
 CC recuperation from chemotherapy, recuperation from irradiation therapy,
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. The present sequence is human DR6 protein.

XX Sequence 655 AA;

Query Match 100.0%; Score 655; DB 23; Length 655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATMTAGSLLGLLSTTTAQPEQKASNLIGTYRHVDRA 60
 DB 1 MGTSPSSSTALASCSRIARRATMTAGSLLGLLSTTTAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFRHENGTEKCHDCSQPCPWPWIEK 120
 DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFRHENGTEKCHDCSQPCPWPWIEK 120
 QY 121 LPCAALTIRECTCPGCMFQSNATCAPHTVCPGVGWVKKGTETEDVRCCKCARGTESDVP 180
 DB 121 LPCAALTIRECTCPGCMFQSNATCAPHTVCPGVGWVKKGTETEDVRCCKCARGTESDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVKPCTKETDNVCGTLPFSSTSPSPGTAFFPRHEMETHE 240
 DB 181 SSVMKCKAYTDCLSQNLVVKPCTKETDNVCGTLPFSSTSPSPGTAFFPRHEMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSTQCTGTPDNTSSARGKEDVKNKLPNLQVNH 300
 DB 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSTQCTGTPDNTSSARGKEDVKNKLPNLQVNH 300
 QY 301 QOGPHRHILKLLPSMEATGGEKSSPTPIKGRKGRHPRQNLKHFDINEHLPWMLVFLLL 360
 DB 301 QOGPHRHILKLLPSMEATGGEKSSPTPIKGRKGRHPRQNLKHFDINEHLPWMLVFLLL 360
 QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTONREKWIYCNHGHDILK 420
 DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTONREKWIYCNHGHDILK 420
 QY 421 LVAAQVGSQWKDIQFCLNASEREVAAFNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 DB 421 LVAAQVGSQWKDIQFCLNASEREVAAFNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 QY 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSRRNGSPFITTEKKDVTLVQVRLDPCDLQPIF 600
 DB 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSRRNGSPFITTEKKDVTLVQVRLDPCDLQPIF 600
 QY 601 DDMHLFNLPEELRVIEEIPQAEKLDRLFEIIGVKSQEAASQTLDSVYSHLPDLL 655
 DB 601 DDMHLFNLPEELRVIEEIPQAEKLDRLFEIIGVKSQEAASQTLDSVYSHLPDLL 655

RESULT 9
 AAY92846

ID AAY92846 standard; Protein; 691 AA.

XX AC AAY92846;

XX DT 29-AUG-2000 (first entry)

XX XX Human osteoprotegrin-like 4 (OPGx4) protein.

XX DE OPGx4; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;

KW inhibitor; bone resorption; vascular calcification; apoptosis;

KW osteopathic.

PD 11-MAR-1999.
 XX 03-SEP-1998; 98WO-US18364.
 XX 04-SEP-1997; 97US-0923725.
 PR 04-SEP-1997; 97US-0057608.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Farrah TM, Gross JA, Matthews SM;
 XX NPI; 1999-205190/17.
 DR W-PSDB; AAX25259.
 XX New secreted or membrane bound tumor necrosis factor receptor
 PT ZTNFR-6 - useful for detecting a genetic abnormality in a patient
 PT Claim 26; Page 113-115; 145pp; English.
 XX The present sequence represents a novel human full-length
 CC membrane-bound tumour necrosis factor receptor, designated ZTNFR-6,
 CC that is characterised by 4 cysteine-rich pseudo-repeat motifs.
 CC ZTNFR-6 polypeptides can be obtained using recombinant techniques.
 CC A polynucleotide (see AAX25259) encoding ZTNFR-6 has been isolated
 CC from an EST database. A secreted, soluble form (see AAY05679) of
 CC ZTNFR-6 has also been identified, which lacks the transmembrane
 CC and cytoplasmic domains of the membrane-bound protein. ZTNFR-6
 CC polypeptides, including the isolated extracellular region,
 CC transmembrane domain and death domain, are claimed. ZTNFR-6
 CC polypeptides are useful in methods that promote cellular maturation
 CC and bone cell regulation. Antibodies raised against ZTNFR-6 are
 CC useful for immunohistochemical tagging of cells expressing ZTNFR-6
 CC for use in diagnosis, isolating ZTNFR-6, generating anti-idiotypic
 CC antibodies, and as neutralising antibodies or antagonists that block
 CC ZTNFR-6 in vivo and in vitro. The polypeptides can also be used to
 CC identify agonists and antagonists of ZTNFR-6. Agonists are useful
 CC for modifying the proliferation and development of target cells in
 CC vitro and in vivo.
 XX Sequence 631 AA;
 SQ
 Query Match 96.3%; Score 631; DB 20; Length 631;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 MIAGSLLLLGFLSTTTTAQPEKASNLIGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNTS 84
 DB 1 MIAGSLLLLGFLSTTTTAQPEKASNLIGTYRHVDRTGQVLTCDKCPAGTYVSEHCTNTS 60
 QY 85 LRVCCSCPVGTFTRHENGIEKCHDCSQPCPWPMPMEKLPKCAALTDRECTCPPGMFQSNATC 144
 DB 61 LRVCCSCPVGTFTRHENGIEKCHDCSQPCPWPMPMEKLPKCAALTDRECTCPPGMFQSNATC 120
 QY 145 APHTVCPVGVKRGKKTETEDVRCKQCARGTFSDFVSSVMKCKAYTDCLSQNLVJTKPGT 204
 DB 121 APHTVCPVGVKRGKKTETEDVRCKQCARGTFSDFVSSVMKCKAYTDCLSQNLVJTKPGT 180
 QY 205 KETDNCVGTLPSSSTSPSPGTAIFRPEHMETHEVPSTYVPKGMNTESSNSASVRP 264
 DB 181 KETDNCVGTLPSSSTSPSPGTAIFRPEHMETHEVPSTYVPKGMNTESSNSASVRP 240
 QY 265 KVLSSIOEGTVDPNTSARGKEDVNTKLPNLQVNVHQGPVHRRHLKLLPSMEATGGEKS 324
 DB 241 KVLSSIOEGTVDPNTSARGKEDVNTKLPNLQVNVHQGPVHRRHLKLLPSMEATGGEKS 300
 QY 325 STPIKPKRGHPQNLKHFIDINEHLPWMIIVLFLVIVVVCSTKRSRTLKKGPROD 384
 DB 301 STPIKPKRGHPQNLKHFIDINEHLPWMIIVLFLVIVVVCSTKRSRTLKKGPROD 360
 QY 385 PSAIVEKAGLKKSMTPTQREKIYYCNGHGIDILKVAQVGSQWKDIYQFLCNASERE 444
 DB 361 PSAIVEKAGLKKSMTPTQREKIYYCNGHGIDILKVAQVGSQWKDIYQFLCNASERE 420

QY 445 VAAFSNGYTADHERAYAAALQHWIRGPEASLAQLISALRQHRNDVVVEKIRGLMEDTTQL 504
 DB 421 VAAFSNGYTADHERAYAAALQHWIRGPEASLAQLISALRQHRNDVVVEKIRGLMEDTTQL 480
 QY 505 ETDKALPMSPLSPSPSPSPNAKLENSALLTVSPSPQDKNGKGFVDESEPLLRCDSTS 564
 DB 481 ETDKALPMSPLSPSPSPSPNAKLENSALLTVSPSPQDKNGKGFVDESEPLLRCDSTS 540
 QY 565 SGSSALSRLNGSFITKEKKDTVLQVRLDPCDLOPIFDDMLHFLNPEELRVIEEIPQAEK 624
 DB 541 SGSSALSRLNGSFITKEKKDTVLQVRLDPCDLOPIFDDMLHFLNPEELRVIEEIPQAEK 600
 QY 625 LDRLEIIGVKSOEASQTLDSVYSHLPDLL 655
 DB 601 LDRLEIIGVKSOEASQTLDSVYSHLPDLL 631
 RESULT 11
 AAE21959
 ID AAE21959 standard; Protein; 631 AA.
 XX AAE21959;
 AC AAE21959;
 XX 25-JUL-2002 (first entry)
 XX Human death domain containing receptor (DR6) protein fragment.
 XX Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
 KW apocytosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
 KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
 KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
 KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
 KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;
 KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
 KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
 KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
 KW dermatologic; hepatotropic; antibacterial.
 XX Homo sapiens.
 XX WC200185209-A2.
 XX 15-NOV-2001.
 XX 30-APR-2001; 2001WO-US11735.
 XX 10-MAY-2000; 2000US-203015P.
 XX (ELIL) LILLY & CO ELI.
 XX Heuer JG, Liu J, Na S, Song HY, Yang D;
 XX WPI; 2002-351283/38.
 XX Treating or preventing T cell or Th2 cell mediated condition e.g.,
 PT asthma or multiple sclerosis in mammal, comprises administering
 PT composition comprising death domain containing receptor, DR6 agonist or
 PT antagonist -
 XX Example 11; Page 129-131; 133pp; English.
 XX The invention relates to a method for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. The
 CC method comprising administering to the mammal a pharmaceutical
 CC composition comprising a death domain containing receptor (DR6) agonist
 CC or antagonist. The method is useful for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
 CC agonist is useful in the manufacture of a medicament for treating or
 CC preventing at least one symptom associated with aberrant apoptosis,
 CC graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma,
 CC atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis,
 CC insulin-dependent diabetes mellitus, cancer, multiple sclerosis, systemic
 CC Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic

CC lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy,
CC autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing
CC lung disease, organ rejection after transplantation, thrombotic
CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
CC for treating or preventing at least one symptom associated with
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
CC infection, complications of infection, human immunodeficiency virus
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
CC associated ulceration, cytoprotection during cancer treatment,
CC recuperation from chemotherapy, recuperation from irradiation therapy,
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. The present sequence is human DR6 protein fragment.

XX
SQ Sequence 631 AA;

Query Match 96.3%; Score 631; DB 23; Length 631;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTS 84
DB 1 MIAGSLLLGLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTS 60

QY 85 LRVSSCPVGTFRHENGIEKCHDCSQPCPMPMEKLPALTDRECTCPGPMFQSNATC 144
DB 61 LRVSSCPVGTFRHENGIEKCHDCSQPCPMPMEKLPALTDRECTCPGPMFQSNATC 120

QY 145 APHTVCPVGWGRKGTETEDVRCKQARGTFSDVPSSVMCKAYTDCLSQNLVYIKPGT 204
DB 121 APHTVCPVGWGRKGTETEDVRCKQARGTFSDVPSSVMCKAYTDCLSQNLVYIKPGT 180

QY 205 KETDNVCGTLPFSFSSSTSPGTAIFPRPEHMETHEVPSSTYVPKGMNSTESNSASVRP 264
DB 181 KETDNVCGTLPFSFSSSTSPGTAIFPRPEHMETHEVPSSTYVPKGMNSTESNSASVRP 240

QY 265 KVLSSIQBGTVPDNTSSARGEDVKNKTLPNQVNVHQGPHRRHLKLLPSMEATGGEKS 324
DB 241 KVLSSIQBGTVPDNTSSARGEDVKNKTLPNQVNVHQGPHRRHLKLLPSMEATGGEKS 300

QY 325 STPIKPRGRHPRQNLKHFEDINEHLPWMIYVLFLLLVIVVCSIRKSSRTLKGPQD 384
DB 301 STPIKPRGRHPRQNLKHFEDINEHLPWMIYVLFLLLVIVVCSIRKSSRTLKGPQD 360

QY 385 PSAIVEKAGLKKSMPTTONREKWIYCYNGHGIDILKLVAAQVGSQWKDIYQFLCNASERE 444
DB 361 PSAIVEKAGLKKSMPTTONREKWIYCYNGHGIDILKLVAAQVGSQWKDIYQFLCNASERE 420

QY 445 VAAFSNGYTAHERAYALQHWITRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL 504
DB 421 VAAFSNGYTAHERAYALQHWITRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL 480

QY 505 ETDKALPMSPLSPSPISPNAKLENSALLTVPEPSQDNKNGFFVDESEPLLCDSTS 564
DB 481 ETDKALPMSPLSPSPISPNAKLENSALLTVPEPSQDNKNGFFVDESEPLLCDSTS 540

QY 565 SGSSALSRLNGSPFITREKKTDLVLRQVRLDPDQLQPIFFDDMLHFLNPEELRVEEIPQAEK 624
DB 541 SGSSALSRLNGSPFITREKKTDLVLRQVRLDPDQLQPIFFDDMLHFLNPEELRVEEIPQAEK 600

QY 625 LDRLEFIIGVKSQEASQILLDSVYSHLPDLL 655
DB 601 LDRLEFIIGVKSQEASQILLDSVYSHLPDLL 631

RESULT 12
AAW75792
ID AAW75792 standard; Protein; 655 AA.

XX
AC AAW75792;
XX
DT 21-DEC-1998 (first entry)
XX
DE Human tumour necrosis factor related receptor TR7.
XX
KW Tumour necrosis factor related receptor; TR7; human; inflammation;
KW arthritis; septicaemia; autoimmune disease; psoriasis;
KW inflammatory bowel disease; infection; graft-versus-host disease;
KW transplant rejection; stroke; acute respiratory disease syndrome;
KW ischaemia; restenosis; brain injury; AIDS; bone disease; cancer;
XX atherosclerosis; Alzheimer's disease; diagnosis; therapy; vaccine.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 24
FT /note= "encoded by ACG"
XX
XX EP869179-A1.
XX
PD 07-OCT-1998.
XX
PF 01-APR-1998; 98EP-0302528.
XX
PR 28-OCT-1997; 97US-0959382.
XX
PR 02-APR-1997; 97US-0041796.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Hurle MR, Tan KB, Young P;
XX
XX WPI: 1998-508493/44.
DR N-PSDB; AAV57441.
XX
PT New tumour necrosis factor receptor TR7 polypeptides and
PT polynucleotides - useful as diagnostic reagents and for treating
XX Alzheimer's disease, AIDS and cancer
XX
PS Claim 11; Page 19-21; 25pp; English.
XX
CC This is the amino acid sequence of a novel member of the human
CC tumour necrosis factor (TNF) receptor superfamily, termed TR7.
CC It was deduced from the coding regions of overlapping isolated
CC cDNA clones (see AAV57441). Expression systems, host cells and a
CC method of producing TR7 polypeptides are claimed. TR7 polypeptides
CC are useful for diagnosing diseases or susceptibility to diseases by
CC determining TR7 polypeptide or mRNA expression. TR7 polypeptide
CC can be used to screen for agonists and antagonists which bind the
CC receptor. These can be used in treatment to inhibit or enhance TR7
CC activity. TR7 antibodies are generated using TR7 polypeptide
CC fragments, and are used for treatment of diseases. TR7 polypeptides
CC and polynucleotides can be administered directly as vaccines for
CC prevention of diseases. Diseases diagnosed, treated or prevented
CC by the above methods include: chronic and acute inflammation,
CC arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel
CC disease, psoriasis), transplant rejection, graft vs. host disease,
CC infection, stroke, ischaemia, acute respiratory disease syndrome,
CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
CC lymphoproliferative disorders), atherosclerosis, and Alzheimer's
XX disease.
XX
SQ Sequence 655 AA;

Query Match 96.3%; Score 631; DB 19; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTS 84
DB 25 MIAGSLLLGLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTS 84

QY 85 LRVCSGCVGTTRHENGIEKCHDCSQCPWPMIEKLPAAALTDRECTCPGFMQSNATC 144
 DB 85 LRVCSGCVGTTRHENGIEKCHDCSQCPWPMIEKLPAAALTDRECTCPGFMQSNATC 144
 QY 145 APHTVCPVGVGVRKKGTTEDVRCKQCARGTFSVPSSVMKCKAYTDCLSNLYVIRPQT 204
 DB 145 APHTVCPVGVGVRKKGTTEDVRCKQCARGTFSVPSSVMKCKAYTDCLSNLYVIRPQT 204
 QY 205 KETDNVCGTLPFSFSSSTSPGTAIFRPRHEMETHVPSTYVPGKMNSTESNSASVYP 264
 DB 205 KETDNVCGTLPFSFSSSTSPGTAIFRPRHEMETHVPSTYVPGKMNSTESNSASVYP 264
 QY 265 KVLSSIQEGTVPDNTSSARGEDVKNLPNLYVNHQOQPHRRHILKLLPSMEATGGEKS 324
 DB 265 KVLSSIQEGTVPDNTSSARGEDVKNLPNLYVNHQOQPHRRHILKLLPSMEATGGEKS 324
 QY 325 STPIKGRKRGHPRQNLKHFDINEHLPWMIIVFLVLLVTVVCSIRKSSRTLKKGPRQD 384
 DB 325 STPIKGRKRGHPRQNLKHFDINEHLPWMIIVFLVLLVTVVCSIRKSSRTLKKGPRQD 384
 QY 385 PSAIVEKAGLKSMPTQNRKWKTYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASERE 444
 DB 385 PSAIVEKAGLKSMPTQNRKWKTYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASERE 444
 QY 445 VAFSNGYTADHERAYAAALQHTWIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTQL 504
 DB 445 VAFSNGYTADHERAYAAALQHTWIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTQL 504
 QY 505 ETDKLALPMSPLSPSPISPNNAKLENSALLTVPEPQDNKGFVDESEPLLRCDSTS 564
 DB 505 ETDKLALPMSPLSPSPISPNNAKLENSALLTVPEPQDNKGFVDESEPLLRCDSTS 564
 QY 565 SGSSALSRNGSFITKEKKDVLROVRLDPCDLQIFDDMLHFLNPEELRVIEEIPQAEK 624
 DB 565 SGSSALSRNGSFITKEKKDVLROVRLDPCDLQIFDDMLHFLNPEELRVIEEIPQAEK 624
 QY 625 LDRLEFIIGVKSQASQTLSDSVSHLPDLL 655
 DB 625 LDRLEFIIGVKSQASQTLSDSVSHLPDLL 655

RESULT 13

AAB44249

ID AAB44249 standard; Protein; 655 AA.

AC AAB44249;

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PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX (GETH) GENENTECH INC.
 XX
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WJ;
 XX
 XX WPI: 2000-611443/58.
 DR N-PSDB: AAC78474.
 DR
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities
 XX
 XX Claim 12; Fig 26; 636pp; English.
 PS
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 655 AA;
 Query Match 84.6%; Score 554; DB 21; Length 655;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTAAPEQKASNLIGTVRRHVDRA 60
 DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTAAPEQKASNLIGTVRRHVDRA 60
 QY 61 TGOVLTCDCPCAGTYVSEHCNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMIEK 120
 DB 61 TGOVLTCDCPCAGTYVSEHCNTSLRVCSSCPVGTFRHENGIEKCHDCSQCPWPMIEK 120
 QY 121 LPCAALTDRECTCPGFMQSNATCAPHTVCPVGVGVRKKGTTEDVRCKQCARGTFSVDP 180
 DB 121 LPCAALTDRECTCPGFMQSNATCAPHTVCPVGVGVRKKGTTEDVRCKQCARGTFSVDP 180
 QY 181 SSVMKCKAYTDCLSQNLVWIKPCTKEDTNVCGTLPFSFSSSTSPGTAIFRPRHEMETH 240
 DB 181 SSVMKCKAYTDCLSQNLVWIKPCTKEDTNVCGTLPFSFSSSTSPGTAIFRPRHEMETH 240
 QY 241 VPSTYVPGKMNSTESNSASVPRKVLSSIQEGTVPDNTSSARGEDVKNLPNLYVNH 300
 DB 241 VPSTYVPGKMNSTESNSASVPRKVLSSIQEGTVPDNTSSARGEDVKNLPNLYVNH 300
 QY 301 QQGPPIHRLKLLPSMEATGGEKSSSTPIKPKRGHPQNLKHFDINEHLPWMIIVFLFLL 360
 DB 301 QQGPPIHRLKLLPSMEATGGEKSSSTPIKPKRGHPQNLKHFDINEHLPWMIIVFLFLL 360
 QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKSMPTQNRKWKTYCNGHGIDILK 420
 DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKSMPTQNRKWKTYCNGHGIDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASEREVAFSNGYTADHERAYAAALQHTWIRGPEASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYQFLCNASEREVAFSNGYTADHERAYAAALQHTWIRGPEASLAQLIS 480

XX 26-JUN-2001 (first entry)
XX Human protein sequence SEQ ID NO:11787.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-0116126.
XX 29-JUL-1999; 99JP-0248036.
XX 27-AUG-1999; 99JP-0300253.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Salto K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX Claim 8; SEQ ID 11787; 2537pp + CD ROM; English.
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
XX AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.

Query Match 82.6%; Score 541; DB 22; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATMTAGSLLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
Db 1 MGTSPSSSTALASCSRIARRATATMTAGSLLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCPWPWIEK 120
Db 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFTRHENGIEKCHDCSQPCPWPWIEK 120
QY 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWVRKKGCTETEDVRCKQCARGTFSVP 180

Db 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWVRKKGCTETEDVRCKQCARGTFSVP 180
QY 181 SSVNKKCKAYTDCLSQNLVWIKPGTKETDNDVCGTILPSFSSSTSPSGTAIPPRHEMETH 240
Db 181 SSVNKKCKAYTDCLSQNLVWIKPGTKETDNDVCGTILPSFSSSTSPSGTAIPPRHEMETH 240
QY 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSTQEGTVPDNTSSARGKEDVNKTLNQLQVNH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSTQEGTVPDNTSSARGKEDVNKTLNQLQVNH 300
QY 301 QQGPHERHILKLLPSMEATGGEKSSSTPIKGPKRGRHPRQNLKHFDINEHLPMWIVLFLLL 360
Db 301 QQGPHERHILKLLPSMEATGGEKSSSTPIKGPKRGRHPRQNLKHFDINEHLPMWIVLFLLL 360
QY 361 VLVVIVVCSIRKSSRTLKKGPRODPSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILK 420
Db 361 VLVVIVVCSIRKSSRTLKKGPRODPSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILK 420
QY 421 LVAAQVGSOWKDIYQFLCNASEREVAAFNSNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Db 421 LVAAQVGSOWKDIYQFLCNASEREVAAFNSNGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540
Db 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540
QY 541 SPQDKNKGFFVDESEPLLRCDSTSSGSSALSRRNGSFTITREKKTDLRQLRDLPCDLQPIF 600
Db 541 SPQDKNKGFFVDESEPLLRCDSTSSGSSALSRRNGSFTITREKKTDLRQLRDLPCDLQPIF 600
QY 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQT 642
Db 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQT 642

Search completed: July 11, 2003, 15:53:15
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:50:18 ; Search time 15 seconds
(without alignments)

1811.133 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTPSPSSSTALASCSRIARR.....SQEASQTLLDSVYSHLPDLL 655

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	655	1	TR21_HUMAN
2	111	16.9	655	1	TR21_MOUSE
3	8	1.2	180	1	HM12_CAEL
4	8	1.2	407	1	YAE1_SCHPO
5	8	1.2	503	1	Y21_HPV21
6	8	1.2	507	1	YG46_YEAST
7	8	1.2	555	1	GP1_CHLRE
8	8	1.2	806	1	TRAL_MAIZE
9	8	1.2	987	1	EPB4_HUMAN
10	8	1.2	1251	1	YG03_CAEL
11	7	1.1	129	1	YVBH_BAGSU
12	7	1.1	135	1	INL5_MOUSE
13	7	1.1	161	1	19KD_MYCAV
14	7	1.1	178	1	X319_MYCG
15	7	1.1	188	1	DSBE_YERPE
16	7	1.1	194	1	TDX_FASHE
17	7	1.1	198	1	Y511_ROTUV
18	7	1.1	207	1	UB6B_MOUSE
19	7	1.1	223	1	NK12_MOUSE
20	7	1.1	227	1	RISB_ARATH
21	7	1.1	231	1	SGBE_HAEIN
22	7	1.1	245	1	MCT1_SHEEP
23	7	1.1	251	1	CRB1_HUMAN
24	7	1.1	251	1	MCT3_SHEEP
25	7	1.1	253	1	C1QB_MOUSE
26	7	1.1	266	1	BLO7_ECOLI
27	7	1.1	270	1	YB62_MYCPN
28	7	1.1	303	1	MURB_BAGSU
29	7	1.1	311	1	CC23_TRYBB
30	7	1.1	348	1	YX99_MYCTU
31	7	1.1	357	1	MYCM_HUMAN
32	7	1.1	360	1	UX0A_THEMA
33	7	1.1	369	1	Y519_CAEL

RESULT 1

ID	TR21_HUMAN	STANDARD	PRT	655 AA
AC	O75509	O96D86		
DT	15-JUN-2002	(Rel. 41, Created)		
DT	15-JUN-2002	(Rel. 41, Last sequence update)		
DE	Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6) (Death receptor 6).			
GN	TNFRSF21 OR DR6			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606			
RP	SEQUENCE FROM N.A.			
RA	Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;			
RT	"Identification and functional characterization of DR6, a novel death domain-containing TNF receptor."			
RL	FEBS Lett. 431:351-356(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Parker A.;			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	TISSUE=Brain, and Colon;			
RL	Strausberg R.;			
CC	Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.			
CC	-!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.			
CC	-!- SUBUNIT: Associates with TRADD.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).			
CC	-!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.			
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.			
CC	-----			
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CC	-----			
DR	EMBL; AF068868; AAC34583.1; -			
DR	EMBL; AL096801; CAB75692.1; -			
DR	EMBL; BC017730; AAH17730.1; -			
DR	EMBL; BC010241; AAH10241.1; ALT_INIT.			
DR	Genew; HGNC:13469; TNFRSF21.			

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DR MW: 605732;
DR HSP: O14763; IDOG.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 100.0%; Score 655; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSALASCRIARRATMTAGSLLGLFLSTTTTAQPEQKASNLGTYRHVDRA 60
DB 1 MGTSPSSALASCRIARRATMTAGSLLGLFLSTTTTAQPEQKASNLGTYRHVDRA 60

QY 61 TGOVLTCDKCPAGTVVSEHCTNTSLRVSCSCPVGTFTRHENGIEKCHDCSQPCWPMEIK 120
DB 61 TGOVLTCDKCPAGTVVSEHCTNTSLRVSCSCPVGTFTRHENGIEKCHDCSQPCWPMEIK 120

QY 121 LFCALTDRETCPCPGMFOGNSATCAPHTVCPGVGWGRKKGTTEDVRCKQCARGTFSVDP 180
DB 121 LFCALTDRETCPCPGMFOGNSATCAPHTVCPGVGWGRKKGTTEDVRCKQCARGTFSVDP 180

QY 181 SSMKCKAYTDCLSQNLVYKGTETDNVCGTLPFSFSSSTSPSGCTAIFPRPEHMETHE 240
DB 181 SSMKCKAYTDCLSQNLVYKGTETDNVCGTLPFSFSSSTSPSGCTAIFPRPEHMETHE 240

QY 241 VPSSTVYVPGMNSTESNSASVRPKVLLSIOBQETVPDNTSSARGEDVNKTLPLNQVNH 300
DB 241 VPSSTVYVPGMNSTESNSASVRPKVLLSIOBQETVPDNTSSARGEDVNKTLPLNQVNH 300

QY 301 QGPHRHRLTKLLPSNEATGGKSTPIKGRGRHPRQNLHFKHFDINEHLPWMIVFLLL 360
DB 301 QGPHRHRLTKLLPSNEATGGKSTPIKGRGRHPRQNLHFKHFDINEHLPWMIVFLLL 360

QY 361 VLWVIVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQONREKIYCNHGHDILK 420
DB 361 VLWVIVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQONREKIYCNHGHDILK 420

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QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSGNGYTADHERAYAAALQHWITRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSGNGYTADHERAYAAALQHWITRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540

QY 541 SPQDNKNGFFVDESEPLLCDDSTSSGSSALSRNGSFITTEKKDVTUQVRLQVLPDCLQPIF 600
DB 541 SPQDNKNGFFVDESEPLLCDDSTSSGSSALSRNGSFITTEKKDVTUQVRLQVLPDCLQPIF 600

QY 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIGVKSQEASQTLDSVYSHLPDLL 655
DB 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIGVKSQEASQTLDSVYSHLPDLL 655

RESULT 2
TR21_MOUSE STANDARD; PRT; 655 AA.
AC Q9EPUS: Q9LXH9; Q91W77;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
(DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT "Murine DR6: murine TNFR-related death receptor-6.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION
RX MEDLINE=21571606; PubMed=11714751;
RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell
differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448(2001).
CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
similarity). May activate JNK and be involved in T-cell
differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -!- May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
thymus, testis, prostate, ovary, small intestine, colon, brain,
lung and kidney, and in fetal brain, liver and lung. Detected at
lower levels in adult peripheral blood leukocytes, lung, and in
fetal muscle, heart, kidney, small intestine and skin. Detected in
T-cells, B-cells and monocytes. In T-cells expression is highest
in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.

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DR EMBL; AF322069; AAG38115.1; -
DR EMBL; AY043489; AAK74193.1; -
DR EMBL; BC016420; AAHL6420.1; -
DR HSSP; O14763; IDOG.
DR MGD; MGI:2151075; Tnfrsf21.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT FT 42 655
FT FT 42 655
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
FT CONFLICT 352 352
FT CONFLICT 523 523
SQ SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99EFF7 CRC64;
Query Match 16.9%; Score 111; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 1.9e-102;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 412 NGHGIDILKLVAAQVGSGWKDIYQFLCNASREVAAFNSGYTADHERAYAAALQHWITIRGP 471
DB 412 NGHGIDILKLVAAQVGSGWKDIYQFLCNASREVAAFNSGYTADHERAYAAALQHWITIRGP 471
QY 472 EASLAQLISALRHRNRDVEKIRGLMEDTTQLETDKALPMSPLSPSP 522
DB 472 EASLAQLISALRHRNRDVEKIRGLMEDTTQLETDKALPMSPLSPSP 522
RESULT 3
ID HM12 CAEEL STANDARD; PRT; 180 AA.
AC P17487; Q9TZZ7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein ceh-12.
GN CEH-12 OR F33D11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Sammons L., Wohlmann P., Mullen G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 154-180 FROM N.A.
RX MEDLINE=90245646; PubMed=1970877;
RA Schaller D., Wittmann C., Spicher A., Mueller F., Tobler H.;
RT "Cloning and analysis of three new homeobox genes from the nematode
Caenorhabditis elegans";
RL Nucleic Acids Res. 18:2033-2036(1990).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
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CC EMBL; AF039720; AAB96698.1; -
DR EMBL; X17076; CAA34928.1; -
DR PIR; S09504; S09504.
DR WormPep; F33D11.4; CE09894.
DR HSSP; P02836; IENH.
DR TRANSFAC; T02987; -
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_repressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT DNA_BIND 110 169
FT HOMEBOX.
SQ SEQUENCE 180 AA; 20296 MW; FC2117756F8D4376 CRC64;
Query Match 1.2%; Score 8; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 216 SFSSSTSP 223
DB 63 SFSSSTSP 70
RESULT 4
YAEI_SCHPO STANDARD; PRT; 407 AA.
ID YAEI_SCHPO
AC Q09842;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C23D3.01 in chromosome I.
GN SPAC23D3.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
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CC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Spouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Pearson D., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Drano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovskii G.V., Ussery D., Barrett B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: TO S.POMBE SPBC215.07C.
CC -1- SIMILARITY: CONTAINS 1 PWMP DOMAIN.
CC
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CC
CC EMBL; Z64354; CAA91236.1; -
DR InterPro; IPR000313; PWMP_domain.
DR Pfam; PF00855; PWMP; 1.
DR SMART; SM00293; PWMP; 1.
DR PROSITE; PS50812; PWMP; 1.
KW Hypothetical protein.
FT DOMAIN 63 129 PWMP.
SQ SEQUENCE 407 AA; 46856 MW; CBB82BDS5CA78A028 CRC64;

Query Match 1.2%; Score 8; DB 1; Length 407;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 SPSPISPSP 526
DB 236 SPSPISPSP 243

RESULT 5
VE2_HPV21
ID VE2_HPV21 STANDARD; PRT; 503 AA.
AC P50767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Regulatory protein E2.
GN E2.
OS Human papillomavirus type 21.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

OX NCBI_TaxID=31548;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; U31779; AAA79397.1; -
DR HSPSP; P03122; 2BOP
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00508; E2_N; 1.
DR Pfam; PF00511; E2_C; 1.
DR ProDom; PD000672; E2_C; 1.
DR ProDom; PD000678; E2_N; 1.
DR ProDom; PD000678; E2_N; 1.
SQ SEQUENCE 503 AA; 56750 MW; AE72A9DF63367266 CRC64;

Query Match 1.2%; Score 8; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 SSSTSPPSP 225
DB 367 SSSTSPPSP 374

RESULT 6
YG46_YEAST
ID YG46_YEAST STANDARD; PRT; 507 AA.
AC P53301;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 52.8 kDa protein in BUB1-HiPI intergenic region.
GN YGK189C OR G7553.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9288C;
RX MEDLINE=97279231; PubMed=9133739;
RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
RA Nombela C.;
RA "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
RT of Saccharomyces cerevisiae chromosome VII."
RL Yeast 13:357-363(1997).
CC -1- SIMILARITY: SOME, TO YEAST UTR2.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z72974; CAA97215.1; -
DR EMBL; X99074; CAA67525.1; -
DR HSPSP; P23904; IAJK.
DR SGD; S0003421; CRH1.
DR InterPro; IPR000757; Glyco_hydro_16.
DR Pfam; PF00722; Glyco_hydro_16; 1.
KW Hypothetical protein.
FT DOMAIN 63 66 POLY-SER.

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FT DOMAIN 301 310 POLY-SER.
FT DOMAIN 345 357 POLY-SER.
FT DOMAIN 387 391 POLY-SER.
FT DOMAIN 467 470 POLY-SER.
SQ SEQUENCE 507 AA; 52757 MW; 7D7B61F57AEA942C CRC64;

Query Match 1.2%; Score 8; DB 1; Length 507;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
DB 356 TSPSSSTA 363

RESULT 7
GPI_CHLRE
ID GPI_CHLRE STANDARD; PRT; 555 AA.
AC Q9FPQ6; Q03927;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vegetative cell wall protein gp1 precursor (Hydroxyproline-rich
DE glycoprotein 1).
GN GPI.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21159092; PubMed=11258910;
RA Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
RA Goodenough U.W.;
RT "Glycosylated prolipoline II rods-with-kinks as a structural motif in
RT plant hydroxyproline-rich glycoproteins.";
RL Biochemistry 40:2978-2987(2001).
RN [2]
RP PARTIAL PRELIMINARY SEQUENCE FROM N.A.
RX MEDLINE=91017504; PubMed=1699225;
RA Adair W.S., Apt K.E.;
RT "Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
RT encoding cell wall hydroxyproline-rich glycoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
CC -!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
CC layer.
CC -!- SUBUNIT: Associates with GP2 and GP3.
CC -!- PTM: N-glycosylated and O-glycosylated.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF309494; AAG45420.1; -
CC EMBL; M58496; AAG69706.1; ALT_SEQ.
CC GlycoSuiteDB; Q9FPQ6; -
CC InterPro; IPR002965; P_rich_extensin.
CC InterPro; IPR003882; Pistill_extensin.
CC PRINTS; PR01217; PRICHEXTENS.
CC PRINTS; PR01218; PSTLEXTENSIN.
CC Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 555 VEGETATIVE CELL WALL PROTEIN GPI.
FT DOMAIN 40 339 49 X 5 AA APPROXIMATE PPSPX REPEATS.
FT DOMAIN 259 279 POLY-PRO.
FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 555 AA; 54219 MW; 6A584A90465502F5 CRC64;
```

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Query Match 1.2%; Score 8; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 SPSPISP 526
DB 366 SPSPISP 373

RESULT 8
TRAIL_MAIZE
ID TRAIL_MAIZE STANDARD; PRT; 806 AA.
AC P08770;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Putative AC transposase (ORFA).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunze R., Stochaj U., Laufs J., Starling P.;
RT "Transcription of transposable element Activator (Ac) of Zea mays L.";
RL EMBO J. 6:1555-1563(1987)
CC -!- MISCELLANEOUS: THIS PROTEIN IS CODED BY THE TRANSPOSABLE MAIZE
CC CONTROLLING ELEMENT "ACTIVATOR" (AC), WHICH IS ABLE TO ACTIVATE
CC CHROMOSOME BREAKAGE AT A SPECIFIC LOCATION; IT MAY BE THE
CC STRUCTURAL GENE FOR A TRANS-ACTING FUNCTION REQUIRED FOR
CC TRANSPOSITION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X05424; CAA29005.1; -
CC MaizEDB; 65747; -
CC InterPro; IPR003656; BED_finger.
CC Pfam; PF02892; zf-BED; 1.
CC Transposable element; Transposition; DNA-binding; DNA recombination;
CC Repeat.
FT INIT_MET 0 0
FT DOMAIN 108 127 10 X 2 AA TANDEM REPEATS OF P-[QE].
SQ SEQUENCE 806 AA; 91890 MW; B3B2B5BE79D53DED CRC64;

Query Match 1.2%; Score 8; DB 1; Length 806;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
DB 68 TSPSSSTA 75

RESULT 9
EPB4_HUMAN
ID EPB4_HUMAN STANDARD; PRT; 987 AA.
AC P54760; Q9BXP0; Q9BTA5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-B receptor 4 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor HTK).
GN EPB4 OR HTK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94245746; PubMed=8186704;
 RA Bennett B.D., Wang Z., Kuang W.J., Wang A., Groopman J.E.,
 RA Goeddel D.V., Scadden D.T.;
 RT "Cloning and characterization of HTK, a novel transmembrane tyrosine
 RT kinase of the EPH subfamily.";
 RL J. Biol. Chem. 269:14211-14218(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [3]
 RN SEQUENCE OF 143-987 FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
 CC EPHRIN-B2. MAY HAVE A ROLE IN EVENTS MEDIATING DIFFERENTIATION AND
 CC DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PLACENTA AND IN A
 CC RANGE OF PRIMARY TISSUES AND MALIGNANT CELL LINES. EXPRESSED IN
 CC FETAL, BUT NOT ADULT, BRAIN, AND IN PRIMITIVE AND MYELOID, BUT NOT
 CC LYMPHOID, HEMATOPOIETIC CELLS.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; U07695; AAA20598.1; -;
 DR EMBL; AF312032; AAK21010.1; -;
 DR EMBL; BC004264; AAH04264.1; -;
 DR HSP; P29323; 1B4F.
 DR Genew; HGNC:3395; EPHB4.
 DR MTM; 600011; -;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FN_III_repeat.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR Pfam; PF01404; EPH_lbd; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PROSITE; PS00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.

DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 987 EPHRIN TYPE-B RECEPTOR 4.
 FT DOMAIN 16 539 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 540 560 POTENTIAL.
 FT DOMAIN 561 987 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 184 320 CYS-RICH.
 FT DOMAIN 321 429 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 430 528 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 615 899 PROTEIN KINASE.
 FT DOMAIN 907 971 SAM.
 FT SITE 985 987 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 621 629 ATP (BY SIMILARITY).
 FT BINDING 647 647 ATP (BY SIMILARITY).
 FT ACT_SITE 740 740 BY SIMILARITY.
 FT MOD_RES 590 590 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 774 774 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 924 924 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 426 426 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 62 62 D -> E (IN REF. 1).
 FT CONFLICT 308 308 Y -> D (IN REF. 1).
 FT CONFLICT 464 464 V -> W (IN REF. 1).
 FT CONFLICT 926 927 ES -> AR (IN REF. 1).
 SQ SEQUENCE 987 AA; 108269 MW; 11A004622F194706 CRC64;

Query Match 1.2%; Score 8; DB 1; Length 987;
 Best Local Similarity 100.0%; Pred No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 LVLVWIV 367
 D6 551 LVLVWIV 558

RESULT 10

YQJ3_CABEL
 ID YQJ3_CABEL STANDARD; PRT; 1251 AA.
 AC Q09550;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypothetical 133.5 kDa protein F26C11.3 in chromosome II.
 GN F26C11.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Matthews P.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----

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CC -----
DR EMBL; Z47072; CAA87369.1;
DR WormPep; F26C11.3; CE01561.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 1.
DR SMART; SM00032; CCP; 1.
KW Hypothetical protein.
FT DOMAIN 120 414
SQ SEQUENCE 1251 AA; 133498 MW; 2B959ECA03B9954A CRC64;

Query Match 1.2%; Score 8; DB 1; Length 1251;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
DB 850 TSPSSSTA 857
|||||||

RESULT 11
YVBH_BAGSU
ID YVBH_BAGSU STANDARD; PRT; 129 AA.
AC P37496;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yybh.
GN YVBH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RY Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RY Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RY Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RY Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RY Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RY Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RY Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RY Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RY Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RY Ghm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RY Guisepi G., Guy B.J., Haga K., Halech K., Harwood C.R., Henaut A.,
RY Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RY Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RY Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RY Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RY Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RY Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RY Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RY Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RY Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RY Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RY Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RY Sekiguchi J., Sekowska A., Seror S.J., Serfor P., Shin B.S., Soldo B.,
RY Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RY Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RY Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RY Viari A., Wambutt R., Wedler H., Weitzenecker T.,
RY Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RY Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
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RL Nature 390:249-256(1997).
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CC -----
DR EMBL; D26185; BAA05195.1;
DR EMBL; Z99124; CAB16101.1;
DR Subtilist; BG10023; yvbh.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 129 AA; 14570 MW; 8FA28AC16BA82E87 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 640 SQTLLDS 646
DB 83 SQTLLDS 89
|||||||

RESULT 12
INL5_MOUSE
ID INL5_MOUSE STANDARD; PRT; 135 AA.
AC Q9WUG6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSL5 precursor (Insulin-like peptide 5)
DE (Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
GN INSL5 OR ZINS3 OR RIF2 OR RIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Colon;
RX MEDLINE=99389725; PubMed=10458910;
RY Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
RY Lok S., Jaspers S.;
RY "Identification of INSL5, a new member of the insulin superfamily.";
RL Genomics 60:50-56(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB; TISSUE=Ovary;
RX MEDLINE=20065648; PubMed=10598589;
RY Hsu S.Y.;
RY "Cloning of two novel mammalian paralogs of relaxin/insulin family
RY proteins and their expression in testis and kidney.";
RL Mol. Endocrinol. 13:2163-2174(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RY Strausberg R.;
RY Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
CC DEVELOPMENT AND REGULATION.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN COLON WITH LOWER LEVELS
CC IN THYMUS. MINIMAL LEVELS IN TESTIS.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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EMBL; AF133817; AAD29687.1; -
EMBL; AF076971; AAD48089.1; -
EMBL; AF054842; AAF09093.1; ALT_INIT.
EMBL; AF054843; AAF09094.1; -
EMBL; BC010968; AAH10968.1; -
MGD; MGI:1346085; Insl5.
InterPro; IPR004825; Ins/IGF/relax.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
insulin family; Hormone; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 135 INSULIN-LIKE PROTEIN INSL5 B CHAIN
(POTENTIAL).
FT PROPEP 49 114 CONNECTING PEPTIDE (POTENTIAL).
FT CHAIN 115 135 INSULIN-LIKE PEPTIDE INSL5 A CHAIN
(POTENTIAL).
FT DISULFID 29 122 INTERCHAIN (BY SIMILARITY).
FT DISULFID 41 135 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 126 BY SIMILARITY.
SQ SEQUENCE 135 AA; 15524 MW; 05FF9A0F613DBF92 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LFLLLVL 362
|||||||
DB 8 LFLLLVL 14

RESULT 13
19KD_MYCAV STANDARD; PRT; 161 AA.
AC P46733;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE 19 kDa lipoprotein antigen precursor.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 2;
RX MEDLINE=933202760; PubMed=8454357;
RA Booth R.J., Williams D.L., Moudgil K.D., Noonan L.C.,
Grandison P.M., McKee J.J., Prestidge R.L., Watson J.D.;
"Homologs of Mycobacterium leprae 18-kilodalton and Mycobacterium
tuberculosis 19-kilodalton antigens in other mycobacteria";
RL Infect. Immun. 61:1509-1515(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Probable).
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM 19 kDa ANTIGEN.
CC
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EMBL; L12235; AAA25346.1; -
DR InterPro; IPR000437; ProLipoprot.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
KW Antigen; Membrane; Lipoprotein; Signal.
FT SIGNAL 1 21 PROBABLE.
FT CHAIN 22 161 19 kDa LIPOPROTEIN ANTIGEN.
FT LIPID 22 161 N-ACYL DIGLYCERIDE (PROBABLE).

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EMBL; AF133817; AAD29687.1; -
EMBL; AF076971; AAD48089.1; -
EMBL; AF054842; AAF09093.1; ALT_INIT.
EMBL; AF054843; AAF09094.1; -
EMBL; BC010968; AAH10968.1; -
MGD; MGI:1346085; Insl5.
InterPro; IPR004825; Ins/IGF/relax.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
insulin family; Hormone; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 135 INSULIN-LIKE PROTEIN INSL5 B CHAIN
(POTENTIAL).
FT PROPEP 49 114 CONNECTING PEPTIDE (POTENTIAL).
FT CHAIN 115 135 INSULIN-LIKE PEPTIDE INSL5 A CHAIN
(POTENTIAL).
FT DISULFID 29 122 INTERCHAIN (BY SIMILARITY).
FT DISULFID 41 135 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 126 BY SIMILARITY.
SQ SEQUENCE 135 AA; 15524 MW; 05FF9A0F613DBF92 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LFLLLVL 362
|||||||
DB 8 LFLLLVL 14

RESULT 13
19KD_MYCAV STANDARD; PRT; 161 AA.
AC P46733;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE 19 kDa lipoprotein antigen precursor.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 2;
RX MEDLINE=933202760; PubMed=8454357;
RA Booth R.J., Williams D.L., Moudgil K.D., Noonan L.C.,
Grandison P.M., McKee J.J., Prestidge R.L., Watson J.D.;
"Homologs of Mycobacterium leprae 18-kilodalton and Mycobacterium
tuberculosis 19-kilodalton antigens in other mycobacteria";
RL Infect. Immun. 61:1509-1515(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Probable).
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM 19 kDa ANTIGEN.
CC
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EMBL; L12235; AAA25346.1; -
DR InterPro; IPR000437; ProLipoprot.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
KW Antigen; Membrane; Lipoprotein; Signal.
FT SIGNAL 1 21 PROBABLE.
FT CHAIN 22 161 19 kDa LIPOPROTEIN ANTIGEN.
FT LIPID 22 161 N-ACYL DIGLYCERIDE (PROBABLE).

SQ SEQUENCE 161 AA; 15504 MW; 78A180B1A1C100E4 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 SSSTSPS 224
|||||||
DB 36 SSSTSPS 42

RESULT 14
Y319_MYCGE STANDARD; PRT; 178 AA.
ID Y319_MYCGE
AC P47561;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG319.
GN MG319.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96011386; PubMed=7592348;
RA Reddy S.P., Rasmussen W.G., Baseman J.B.;
"Molecular cloning and characterization of an adherence-related
operon of Mycoplasma genitalium";
RL J. Bacteriol. 177:5943-5951(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-P., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium";
RL Science 270:397-403(1995).
RN [3]
RP SEQUENCE OF 34-141 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
sequencing";
RL J. Bacteriol. 175:7918-7930(1993).
CC
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CC or send an email to license@isb-sib.ch).

EMBL; L43097; AAA99944.1; -
DR EMBL; U39712; AAC71541.1; -
DR EMBL; U01769; AAD10587.1; -
DR TIGR; MG319; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
SQ SEQUENCE 178 AA; 20556 MW; 1BCC5FDA9DA4AE14 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 27 secs

Qy 357 FLLLVLV 363
|
Db 12 FLLLVLV 18

RESULT 15

DSBE_YERPE STANDARD; PRT; 188 AA.
AC Q8ZD52;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thiol:disulfide interchange protein dsbe (Cytochrome c biogenesis
DE protein ccmg).
DE DSBE OR CCMG OR YPO2740.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN-CO-92 / Biovar Orientalis;
RC MEDLINE=21470413; PubMed=11586360;
RX Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
CC -!- FUNCTION: Involved in disulfide bond formation. Catalyzes a late,
CC reductive step in the assembly of periplasmic c-type cytochromes,
CC probably the reduction of disulfide bonds of the apocytochrome c
CC to allow covalent linkage with the heme. Possible subunit of a
CC heme lyase (By similarity).
CC -!- SUBCELLULAR LOCATION: Mostly periplasmic; anchored in the inner
CC membrane (By similarity).
CC -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. DSBE SUBFAMILY.CC
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CC -----
CC EMBL; AJ414153; CAC92979.1; -
CC InterPro; IPR004799; Dsbe.
CC InterPro; IPR000063; Thioired.
CC ProDom; PD03679; Dsbe; 1.
CC TIGRFAMs; TIGR00385; dsbe; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
KW Cytochrome c-type biogenesis; Redox-active center; Transmembrane;
KW Inner membrane; Complete proteome.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 POTENTIAL.
FT DOMAIN 31 188 PERIPLASMIC (POTENTIAL).
FT DISULFID 85 88 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 188 AA; 21072 MW; AEA1967477034A56 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 355 VLFLLV 361
|
Db 16 VLFLLV 22

Search completed: July 11, 2003, 15:54:16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:49:42 ; Search time 22 seconds
(without alignments)
2862.184 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTSPSSSTALASCSRIARR.....SQEASQTLLDSVYSHLPDLL 655

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	7.5	651	JC7705	death receptor-6 -
2	9	1.4	387	G82983	probable MFS trans
3	8	1.2	127	S65194	probable membrane
4	8	1.2	138	B27863	Ac hypothetical pr
5	8	1.2	180	T32764	hypothetical prote
6	8	1.2	222	T43500	hypothetical prote
7	8	1.2	271	G83554	hypothetical prote
8	8	1.2	283	D71130	probable oligopept
9	8	1.2	305	C82524	pyrroline-5-carbox
10	8	1.2	312	A82485	iron(III) ABC tran
11	8	1.2	316	AD2470	hypothetical prote
12	8	1.2	407	S62492	hypothetical PMP
13	8	1.2	425	C70450	conserved hypothet
14	8	1.2	485	T24201	hypothetical prote
15	8	1.2	507	S64507	probable membrane
16	8	1.2	647	T42579	capsid protein 35
17	8	1.2	683	T12123	NADH2 dehydrogenas
18	8	1.2	807	T02916	hypothetical prote
19	8	1.2	880	T48477	hypothetical prote
20	8	1.2	987	A54092	protein-tyrosine k
21	8	1.2	1251	T21389	hypothetical prote
22	7	1.1	72	A11026	hypothetical prote
23	7	1.1	86	B75465	probable cation tr
24	7	1.1	103	D72549	hypothetical prote
25	7	1.1	113	T33779	hypothetical prote
26	7	1.1	113	C68947	protein C397.3 [1
27	7	1.1	114	G82793	hypothetical prote
28	7	1.1	119	D84845	hypothetical prote
29	7	1.1	119	H87152	hypothetical prote

30	7	1.1	128	2	JQ1203	hypothetical 14k p
31	7	1.1	129	2	S65989	yybH protein - Bac
32	7	1.1	135	2	G72601	hypothetical prote
33	7	1.1	135	2	C72539	hypothetical prote
34	7	1.1	141	2	T19125	probable transposa
35	7	1.1	143	2	G97752	tolR protein limpo
36	7	1.1	150	2	C87517	DnaJ-related prote
37	7	1.1	151	2	T16284	hypothetical prote
38	7	1.1	158	2	E86396	t2p11.14 protein -
39	7	1.1	160	2	D98138	probable transcrip
40	7	1.1	172	2	AF3149	transcription regu
41	7	1.1	174	2	F84338	hypothetical prote
42	7	1.1	177	2	AE1410	hypothetical prote
43	7	1.1	178	2	C64235	hypothetical prote
44	7	1.1	186	2	AF2205	hypothetical prote
45	7	1.1	188	2	AD0334	thiol,disulfide in

ALIGNMENTS

RESULT 1

JC7705

death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: JC7705

R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, and is involved in cell death and/or survival signaling cascade.

C:Genetics:

A:Gene: dr-6

C:Keywords: ovary

F:1-21/Domain: signal sequence #status predicted <SIG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DED>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 7.5%; Score 49; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 ADHERAYAAHQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTT 502

Db 435 ADHERAYAAHQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTT 483

RESULT 2

G82983

probable MFS transporter PA5311 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G82983

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G82983

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-387 <STO>

A:Cross-references: GB:AE004943; GB:AE004091; NID:G9951615; PIDN:AA080696.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:
A:Gene: PA5311

Query Match 1.4%; Score 9; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 IAGSLLLLG 34
|||||
DB 167 IAGSLLLLG 175

RESULT 3

S65194
probable membrane protein YPL182c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein P2235
C:Species: Saccharomyces cerevisiae
C:Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 19-Apr-2002
A:Accession: S65194
R:Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S65183
A:Accession: S65194
A:Molecule type: DNA
A:Residues: 1-127 <BEN>
A:Cross-references: EMBL:Z73538; NID:g1370380; PID:e246911; PID:g1370381; GSPDB:GN000016;
A:Experimental source: strain S288C (AB972)
C:Genetics:

A:Gene: MIPS:YPL182c
A:Cross-references: SGD:S0006103
A:Map position: 16L
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YPL182c
C:Keywords: transmembrane protein
F:43-59/Domain: transmembrane #status predicted <TM1>
F:90-106/Domain: transmembrane #status predicted <TM2>

Query Match 1.2%; Score 8; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 SSSTSPSP 225
|||||
DB 22 SSSTSPSP 29

RESULT 4

B27863
Ac hypothetical protein ORFa - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Sep-1993
C:Accession: B27863
R:Kunze, R.; Stochaj, U.; Laufs, J.; Starlinger, P.
EMBO J. 6, 1555-1563, 1987
A:Title: Transcription of transposable element Activator (Ac) of Zea mays L.
A:Reference number: A91069
A:Accession: B27863
A:Molecule type: mRNA
A:Residues: 1-138 <KUN>
C:Superfamily: hypothetical transposase Ac9

Query Match 1.2%; Score 8; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10
|||||
DB 69 TSPSSSTA 76

RESULT 5

T32764
hypothetical protein F33D11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32764
R:Sammons, L.; Wohldmann, P.; Mullen, G.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F33D11.
A:Reference number: Z21222
A:Accession: T32764
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-180 <SAM>
A:Cross-references: EMBL:AF039720; PIDN:AB96698.1; GSPDB:GN000019; CESP:F33D11.4
A:Experimental source: strain Bristol N2; clone F33D11
C:Genetics:

A:Gene: CESP:F33D11.4
A:Map position: 1
A:Introns: 68/1; 99/1; 153/3
Query Match 1.2%; Score 8; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 SFSSSTSP 223
|||||
DB 63 SFSSSTSP 70

RESULT 6

T43500
hypothetical protein DKF2p586G1721.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43500
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z22515
A:Accession: T43500
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-222 <AAA>
A:Cross-references: EMBL:AL133642
A:Experimental source: adult uterus; clone DKF2p586G1721
C:Genetics:
A:Note: DKF2p586G1721.1

Query Match 1.2%; Score 8; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 STSPSPGT 227
|||||
DB 140 STSPSPGT 147

RESULT 7

G83554
hypothetical protein PA0735 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83554
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <STO>
A:Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:NAG04124.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0735

RESULT 12

S62492
hypothetical PMP domain-containing protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S62492; T38277
R:Niblett, D.; Harris, D.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62492
A:Accession: S62492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <NIB>
A:Cross-references: EMBL:Z64354; NID:g1039338; PIDN:CAA91236.1; PID:g1039339
R:Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21783
A:Accession: T38277
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-407 <NIB>
A:Cross-references: EMBL:Z64354; PIDN:CAA91236.1; GSPDB:GN00066; SPDB:SPAC23D3.01
A:Gene: SPAC23D3.01
C:Genetics:
A:Experimental source: strain 972h; cosmid c23D3
A:Map position: 1R

Query Match 1.2%; Score 8; DB 2; Length 407;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 SPSPISPSP 526

Db 236 SPSPISPSP 243

RESULT 13

C70450
conserved hypothetical protein aq_1743 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: C70450
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oviatt, J.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70450
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425 <AQF>
A:Cross-references: GB:AE000754; NID:g2984047; PIDN:AAC07601.1; PID:g2984060; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_1743

Query Match 1.2%; Score 8; DB 2; Length 425;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 LLVLVVIV 366

Db 9 LLVLVVIV 16

RESULT 14

T24201
hypothetical protein R12G8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24201
R:Basham, V.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19853

A:Accession: T24201

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-485 <WIL>

A:Cross-references: EMBL:Z93782; PIDN:CAB07854.1; GSPDB:GN00023; CESP:R12G8.2

A:Experimental source: clone R12G8

C:Genetics:

A:Gene: CESP:R12G8.2

A:Map position: 5

A:Introns: 74/1; 162/3; 210/1; 288/1; 339/3; 426/3

Query Match 1.2%; Score 8; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 STSSGSSA 569

Db 397 STSSGSSA 404

RESULT 15

S64507
probable membrane protein YGR189c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G7553
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C:Accession: S64507
R:Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64499
A:Accession: S64507
A:Molecule type: DNA
A:Residues: 1-507 <ARR>

A:Cross-references: EMBL:Z72974; NID:g1323335; PID:e243566; PID:g1323336; GSPDB:GN000

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:CRH1; MIPS:YGR189c

A:Cross-references: SGD:S0003421

A:Map position: 7R

C:Keywords: transmembrane protein

F;6-22/Domain: transmembrane #status predicted <TM>

Query Match 1.2%; Score 8; DB 2; Length 507;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSPSSSTA 10

Db 356 TSPSSSTA 363

Search completed: July 11, 2003, 15:53:46

Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2003, 15:47:53 ; Search time 88 Seconds
(without alignments)
1533.646 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 655

Sequence: 1 MGTPSPSSSTALASCRIARR.....SQBASQTLLDSVYSHLPDLL 655

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	7.5	83	Q8UWJ0	Q8UWJ0 gallus gall
2	49	7.5	651	Q98SM6	Q98SM6 gallus gall
3	9	1.4	387	Q9HTP3	Q9HTP3 pseudomonas
4	9	1.4	3396	Q3VM55	Q9VM55 drosophila
5	8	1.2	120	Q8SAZ1	Q8SAZ1 oryza sativ
6	8	1.2	127	Q8922	Q8922 saccharomyc
7	8	1.2	132	Q943G4	Q943G4 oryza sativ
8	8	1.2	180	Q9TZ27	Q9TZ27 caenorhabdi
9	8	1.2	219	Q9YXH9	Q9YXH9 human immun
10	8	1.2	222	Q4UF25	Q4UF25 homo sapien
11	8	1.2	240	Q98K49	Q98K49 rhizobium 1
12	8	1.2	271	Q9I5J4	Q9I5J4 pseudomonas
13	8	1.2	275	Q69051	Q69051 pseudomonas
14	8	1.2	283	Q58539	Q58539 pyrococcus
15	8	1.2	305	Q9PA08	Q9PA08 xylella fas
16	8	1.2	312	Q9KMU1	Q9KMU1 vibrio chol

17	8	1.2	314	10	O22440	O22440 oryza sativ
18	8	1.2	316	16	Q8YLI2	Q8YLI2 anabaena sp
19	8	1.2	345	10	Q949D2	Q949D2 oryza sativ
20	8	1.2	352	15	Q9WDC4	Q9WDC4 human immun
21	8	1.2	362	4	O95884	O95884 homo sapien
22	8	1.2	393	11	P70429	P70429 mus musculus
23	8	1.2	414	11	Q9ERU8	Q9ERU8 mus musculus
24	8	1.2	416	4	Q9UI08	Q9UI08 homo sapien
25	8	1.2	416	4	Q8TBV1	Q8TBV1 homo sapien
26	8	1.2	418	4	Q9UIC2	Q9UIC2 homo sapien
27	8	1.2	425	16	O67629	O67629 aquifex aeo
28	8	1.2	485	5	Q9XTV6	Q9XTV6 caenorhabdi
29	8	1.2	493	10	Q9LUS8	Q9LUS8 arabidopsis
30	8	1.2	572	11	Q9QZF6	Q9QZF6 rattus norv
31	8	1.2	577	10	Q9EXY7	Q9EXY7 artemisia a
32	8	1.2	586	10	Q94HX6	Q94HX6 oryza sativ
33	8	1.2	617	13	Q9IAA9	Q9IAA9 brachydanio
34	8	1.2	617	13	Q9PU64	Q9PU64 brachydanio
35	8	1.2	647	12	O39278	O39278 equine herp
36	8	1.2	683	8	O46936	O46936 saintpaulia
37	8	1.2	840	5	Q9N3Q5	Q9N3Q5 caenorhabdi
38	8	1.2	880	10	Q9LZ16	Q9LZ16 arabidopsis
39	8	1.2	935	4	Q96L35	Q96L35 homo sapien
40	8	1.2	949	10	Q9FMC9	Q9FMC9 arabidopsis
41	8	1.2	1021	5	Q8T811	Q8T811 dictyosteli
42	7	1.1	43	2	Q9K546	Q9K546 mycobacteri
43	7	1.1	53	2	Q93A11	Q93A11 thiobacillu
44	7	1.1	57	9	O56786	O56786 staphylococ
45	7	1.1	58	5	Q9VB42	Q9VB42 drosophila

ALIGNMENTS

RESULT 1

Q8UWJ0 PRELIMINARY; PRT; 83 AA.
AC Q8UWJ0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Death receptor 6 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA Shi Z., Onagbesan O.M., Williams J.;
RT "Apoptosis in chicken ovary."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432512; AAL35560.1; -
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; Death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9506 MW; 28F8C880F655FADC CRC64;

Query Match 7.5%; Score 49; DB 13; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 ADHERAYALQHWIRGPEASLAQLISALRQHRNDVYKIRGLMEDTT 502

Db 21 ADHERAYALQHWIRGPEASLAQLISALRQHRNDVYKIRGLMEDTT 69

RESULT 2

Q98SM6

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ID Q98SM6 PRELIMINARY; PRT; 651 AA.
AC
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP
SEQUENCE FROM N.A.
AC Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL EMBL: AF349508; AAK29666.2;
DR HSSP; P19438; INCF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR003975; Shal_channel.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 4.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;
Query Match 7.5%; Score 49; DB 13; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 454 ADHERAYALQHWITIRGPASLAQLSALRQHRNDVVEKIRGLMEDTT 502
Db [1]
QY 435 ADHERAYALQHWITIRGPASLAQLSALRQHRNDVVEKIRGLMEDTT 483
RESULT 3
Q9HTP3 PRELIMINARY; PRT; 387 AA.
AC
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable MFS transporter.
GN PA5311.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN [1]
RP
SEQUENCE FROM N.A.
AC STRAIN=ATCC 15692 / PA01;
RC MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goitry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AE004943; AAG08696.1;
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00083; sugar_tr; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
KW Complete proteome.
```

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SQ SEQUENCE 387 AA; 40522 MW; F898F53844EAA00B CRC64;
Query Match 1.4%; Score 9; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 IAGSLLLLG 34
Db [1]
QY 167 IAGSLLLLG 175
RESULT 4
Q9VM55 PRELIMINARY; PRT; 3396 AA.
AC
ID Q9VM55;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG9138 protein.
GN SP1070 OR CG9138.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP
SEQUENCE FROM N.A.
AC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
CC -!- SIMILARITY: CONTAINS 3 CUB DOMAINS.
DR EMBL; AE003615; AAF52472.1;
DR HSSP; P00740; 1EDM.
DR FlyBase; FBgn0031879; SPL070.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
```

DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR001092; HLH_basic.
DR InterPro: IPR003410; Hyalin.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF00008; EGF; 17.
DR Pfam: PF00734; FS_F8_type_C; 2.
DR Pfam: PF02494; HVR; 3.
DR Pfam: PF00057; ldl_recept_a; 1.
DR Pfam: PF00084; sushi; 7.
DR PRINTS: PR00010; EGFBL00D.
DR SMART: SM00032; CCP; 8.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00179; EGF_CA; 8.
DR SMART: SM00001; EGF_like; 9.
DR SMART: SM00231; FA58C; 2.
DR SMART: SM00282; Lang; 1.
DR SMART: SM00192; LDLa; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 11.
DR PROSITE: PS01180; CUB; 6.
DR PROSITE: PS00022; EGF_1; 15.
DR PROSITE: PS01186; EGF_2; 13.
DR PROSITE: PS01187; EGF_CA; 7.
DR PROSITE: PS01285; FA58C_1; 1.
DR PROSITE: PS01209; LDLRA_1; 1.
DR PROSITE: PS00068; LDLRA_2; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 3396 AA; 369389 MW; E618E9ACEA13E0E5 CRC64;

Query Match 1.4%; Score 9; DB 5; Length 3396;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 CPAGTYVSE 78
Db 1694 CPAGTYVSE 1702

RESULT 5

ID Q8SAZ1 PRELIMINARY; PRT; 120 AA.
AC Q8SAZ1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative dimethyladenosine transferase.
GN OSUNBA0029P16.20.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Sasaki C., Henry D., Oates R., Simmons J., Wilson R., Mix P., Du H.;
RT "Rice Genomic Sequence."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC093568; AAL78110.1; -;
SQ SEQUENCE 120 AA; 12304 MW; A31240266825CE58 CRC64;

Query Match 1.2%; Score 8; DB 10; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 388 IVEKAGLK 395
Db 52 IVEKAGLK 59

RESULT 6

ID Q08922 PRELIMINARY; PRT; 127 AA.
AC Q08922;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ORF YPL182C.
GN YPL182C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Nentwich U., Voss H., Ansoorge W.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73538; CAA97890.1; -;
DR SGD: S0006103; YPL182C.
SQ SEQUENCE 127 AA; 13208 MW; A8FB6A243A7F7336 CRC64;

Query Match 1.2%; Score 8; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 SSSTSPSP 225
Db 22 SSSTSPSP 29

RESULT 7

ID Q943G4 PRELIMINARY; PRT; 132 AA.
AC Q943G4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P0046E05.16 protein (P0435B05.2 protein).
GN P0046E05.16 OR P0435B05.2.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0046E05.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0435B05.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003237; BAB67909.1; -;
DR EMBL; AP003249; BAB89525.1; -;
SQ SEQUENCE 132 AA; 12926 MW; C78D583ACB723D31 CRC64;

Query Match 1.2%; Score 8; DB 10; Length 132;

Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 IVEKAGLK 395
Db 81 IVEKAGLK 88

RESULT 8
Q9TZ27 PRELIMINARY; PRT; 180 AA.
ID Q9TZ27;
AC Q9TZ27;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 20.3 kDa protein.
GN F33D11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.,"
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Sammons L., Wohldmann P., Mullen G.;
RT "The sequence of C. elegans cosmid F33D11.,"
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.,"
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF039720; AAB96698.1; -;
DR HSSP; P02836; LENH.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH repressr.
DR Pfam; PF00046; homeobox.1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox.1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX.1; 1.
DR PROSITE; PS00071; HOMEBOX.2; 1.
KW DNA-binding; Homeobox; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 180 AA; 20296 MW; FC2117756F8D4376 CRC64;

Query Match 1.2%; Score 8; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 SFSSSTSP 223
Db 63 SFSSSTSP 70

RESULT 9
Q9YXH9 PRELIMINARY; PRT; 219 AA.
ID Q9YXH9;
AC Q9YXH9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE -Gp120 (Fragment).

GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TZB0041;
RX MEDLINE=98252392; PubMed=9591718;
RA Renjifo B., Chaplin B., Mwakagile D., Shah P., Vannberg F.,
RA Msamanga G., Hunter D., Fawzi W., Essex M.;
RT "Epidemic expansion of HIV type 1 subtype C and recombinant genotypes
in Tanzania.,"
RL AIDS Res. Hum. Retroviruses 14:635-638(1998).
DR EMBL; AF038091; AAC98585.1; -;
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 24128 MW; E8C2187A57842751 CRC64;

Query Match 1.2%; Score 8; DB 15; Length 219;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 MNSTESNS 258
Db 123 MNSTESNS 130

RESULT 10
Q9UF25 PRELIMINARY; PRT; 222 AA.
ID Q9UF25;
AC Q9UF25;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Hypothetical 22.4 kDa protein (Fragment).
GN DKFZP586G1721.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133642; CAB63763.1; -;
DR InterPro; IPR002965; P_rich_extensn.
DR PRINTS; PR01217; PRICHEXTENS.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 222 AA; 22369 MW; D0AF3E9C1C95EF95 CRC64;

Query Match 1.2%; Score 8; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 STSPSPGT 227
Db 140 STSPSPGT 147

RESULT 11
Q98K49 PRELIMINARY; PRT; 240 AA.
ID Q98K49;
AC Q98K49;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Probable oxidoreductase.
GN MLR1638.


```

OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AF002997; BAB48965.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 24974 MW; 32EAF70467197083 CRC64;

Query Match 1.2%; Score 8; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TGOVLTC D 68
DB 226 TGOVLTC D 233

RESULT 12
Q915J4 PRELIMINARY; PRT; 271 AA.
AC Q915J4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA0735.
GN PA0735.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004508; RAG04124.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 271 AA; 30821 MW; FAA5549CD4BD714E CRC64;

Query Match 1.2%; Score 8; DB 16; Length 271;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 IAGSLLLL 33
DB 10 IAGSLLLL 17

RESULT 13
O69051 PRELIMINARY; PRT; 275 AA.
ID O69051

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O69051;
AC 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ATP-binding protein ptxA.
GN PtxA.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WM88;
RX MEDLINE=99008986; PubMed=97911102;
RA Metcalf W.W., Wolfe R.S.;
RT "Molecular genetic analysis of phosphite and hypophosphite oxidation
RT by Pseudomonas stutzeri WM88.";
RL J. Bacteriol. 180:5547-5558(1998).
CC -!- FUNCTION: PROBABLY FORMS PART OF A BINDING-PROTEIN-DEPENDENT
CC PHOSPHITE TRANSPORTER. REQUIRED FOR OXIDATION OF PHOSPHITE TO
CC PHOSPHATE.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF061070; AAC71706.1; -.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR ProSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
FT NP_BIND 44 51 ATP (POTENTIAL).
SQ SEQUENCE 275 AA; 29649 MW; CC057CBE25A5B6BB CRC64;

Query Match 1.2%; Score 8; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 SALRQHR 487
DB 79 SALRQHR 86

RESULT 14
O58539 PRELIMINARY; PRT; 283 AA.
AC O58539;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 283AA long hypothetical oligopeptide transport permease protein APPC.
GN PH0809.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000003; BAA29902.1; -.
DR InterPro; IPR00515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 283 AA; 30664 MW; 922478741D15AF54 CRC64;

Query Match 1.2%; Score 8; DB 17; Length 283;

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Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 LLLVLVVI 365
| | | | | | | |
DB 24 LLLVLVVI 31

RESULT 15

Q9PA08 PRELIMINARY; PRT; 305 AA.
AC Q9PA08; 2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Pyroline-5-carboxylate reductase.
GN XF2712.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuran E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE004077; AAF85509.1; -
DR InterPro: IPR000304; P5CR.
DR Pfam: PF01089; P5CR; 1.
DR TIGRFAMs: TIGR00112; proc; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 31918 MW; BD0803B6FC09AB5 CRC64;

Query Match 1.2%; Score 8; DB 16; Length 305;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 RATATMIA 27
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DB 8 RATATMIA 15

Search completed: July 11, 2003, 15:51:44
Job time : 93 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:44:48 ; Search time 42 Seconds
(without alignments)
2078.075 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

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Scoring table: BLOSUM62

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3456	100.0	655	20 AAY41693	Human PRO868 prote
2	3456	100.0	655	20 AAW81059	Novel human tumor
3	3456	100.0	655	21 AAB26981	Human tumour necro
4	3456	100.0	655	21 AAB01349	Tumour necrosis fa
5	3456	100.0	655	21 AAB01338	DR-6 death recepto
6	3456	100.0	655	21 AAY77460	Human TNF receptor
7	3456	100.0	655	22 AAU29232	Human PRO polypept
8	3456	100.0	655	23 AAE21958	Human death domain
9	3456	100.0	691	21 AAY92846	Human osteoprotegr
10	3454	99.9	655	21 AAB44249	Human PRO868 (UNQ4

11	3450	99.8	655	19 AAW75792	Human tumour necro
12	3444	99.7	655	22 AAB93023	Human protein sequ
13	3342	96.7	631	20 AAY05678	Human full-length
14	3342	96.7	631	23 AAB21959	Human death domain
15	2892	83.7	605	20 AAY05697	Human TNF receptor
16	2723	78.8	573	20 AAY05695	Mouse TNF receptor
17	2573	74.5	508	20 AAY05680	Tumour necrosis fa
18	2544	73.6	600	21 AAY92845	Murine osteoprotegr
19	2233	64.6	444	21 AAY77461	Human TNF receptor
20	2091	60.5	405	21 AAY67947	Human DETH protein
21	2079	60.2	393	20 AAY28450	A human tumour nec
22	1365	39.5	254	21 AAY92843	Human osteoprotegr
23	1359	39.3	253	20 AAY05696	Human TNF receptor
24	1357	39.3	290	21 AAY92844	Human osteoprotegr
25	1354	39.2	290	21 AAY92842	Human osteoprotegr
26	1245	36.0	229	20 AAY05679	Human soluble tumo
27	1216	35.2	222	22 AAY56603	Human brain expres
28	1216	35.2	222	22 AAM16812	Peptide #3246 enco
29	1216	35.2	222	22 AAM29294	Peptide #3331 enco
30	1216	35.2	222	22 AAM04528	Peptide #3210 enco
31	1216	35.2	222	23 AAG38570	Human peptide enco
32	992	28.7	210	21 AAY77459	Human TNF receptor
33	934	27.0	164	21 AAB00012	Peptide fragment o
34	841	24.3	147	21 AAB26985	Human TNF receptor
35	673	19.5	125	19 AAW75793	Tumour necrosis fa
36	439	12.7	85	22 ABB29318	Peptide #1969 enco
37	439	12.7	85	22 ABB30755	Peptide #3406 enco
38	439	12.7	85	22 ABB35932	Peptide #3438 enco
39	439	12.7	85	22 ABB19901	Protein #1900 enco
40	439	12.7	85	22 ABB21341	Protein #3340 enco
41	439	12.7	85	22 AAM55278	Human brain expres
42	439	12.7	85	22 AAM56735	Human brain expres
43	439	12.7	85	22 AAM67675	Human bone marrow
44	439	12.7	85	22 AAM69113	Human bone marrow
45	439	12.7	85	22 AAM15484	Peptide #1918 enco

ALIGNMENTS

RESULT 1

AAY41693
ID AAY41693 standard; Protein; 655 AA.

XX AC AAY41693;

XX DT 07-DEC-1999 (first entry)

XX DE Human PRO868 protein sequence.

XX DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.

XX OS Homo sapiens.

XX PN WO9946281-A2.

XX PD 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1998; 98US-0077450.

XX PR 11-MAR-1998; 98US-0077632.

XX PR 11-MAR-1998; 98US-0077641.

XX PR 12-MAR-1998; 98US-0077649.

XX PR 13-MAR-1998; 98US-0077791.

XX PR 17-MAR-1998; 98US-0078004.

XX PR 20-MAR-1998; 98US-0040220.

XX PR 20-MAR-1998; 98US-0078886.

XX PR 20-MAR-1998; 98US-0078910.

XX PR 20-MAR-1998; 98US-0078936.

XX PR 20-MAR-1998; 98US-0078939.

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 PR 31-MAR-1998; 98US-0079923.
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 PR 29-APR-1998; 98US-0083545.
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 PR 29-APR-1998; 98US-0083558.
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 PR 07-MAY-1998; 98US-0084600.
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 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.

PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX (GETH) GENENTECH INC.
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 DR WPI: 1999-551358/46.
 DR N-PSDB; AA233945.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders
 XX
 PS Claim 12; Fig 26; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA233891 to
 CC AA234338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 655 AA;
 Query Match 100.0%; Score 3456; DB 20; Length 655;
 Best Local Similarity 100.0%; Pred No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTTAQPEKASNLIGTYRHVDRA 60
 DB 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTTAQPEKASNLIGTYRHVDRA 60
 QY 61 TQVLTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFTREHNGIEKHCHDCQCPWPMEIK 120
 DB 61 TQVLTCDKCPAGTYVSEHCTNTSLRVCSGCPVGTFTREHNGIEKHCHDCQCPWPMEIK 120
 QY 121 LFCALTDRETCPCPGMFOFNATCAPHTVCPVGVGWYKKGTEDEVRCKQCARGTSDVP 180
 DB 121 LFCALTDRETCPCPGMFOFNATCAPHTVCPVGVGWYKKGTEDEVRCKQCARGTSDVP 180
 QY 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGCTAIFRPEHMETHE 240
 DB 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGCTAIFRPEHMETHE 240
 QY 241 VPSSTYVPGKMNSTESNSSASVRPKVLLSIIQGTVPDNTSSARGKEDVNKTLPNLQVNVH 300
 DB 241 VPSSTYVPGKMNSTESNSSASVRPKVLLSIIQGTVPDNTSSARGKEDVNKTLPNLQVNVH 300
 QY 301 QOGPHRHILKLLPSMEATGGEKSSPTPIKGRKRGHPQNLKHFDINEHLPWMVILFLLL 360
 DB 301 QOGPHRHILKLLPSMEATGGEKSSPTPIKGRKRGHPQNLKHFDINEHLPWMVILFLLL 360
 QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSWPTTONREKWIYYCNGHGDILK 420
 DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSWPTTONREKWIYYCNGHGDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNGYTADHERAYAAALQHTTIRGPASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNGYTADHERAYAAALQHTTIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSSGSSSALSRNGSFITKEKKDTVLQRVRLDPCDLQPIF 600

Db 541 SPQDKNGFFVDESEPLRLCDSTSSGSSALSRSNGSFITKEKQTVLRQVRLDPCDLQPIF 600
 Qy 601 DDMHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSYSHLPDLL 655
 Db 601 DDMHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSYSHLPDLL 655

RESULT 2

AAW81059
 ID AAW81059 standard; Protein: 655 AA.
 AC AAW81059;
 XX 10-MAY-1999 (first entry)
 DT Novel human tumor necrosis factor receptor TR9.
 DE Human; tumour necrosis factor receptor; TNFR; TR9 receptor; cancer;
 KW apoptosis; agonist; inhibition; autoimmune disorder; viral infection;
 KW inflammation; antagonist; AIDS; neurodegenerative disorder.
 XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..40
Peptide	/note= "signal peptide"
Peptide	41..655
Peptide	/note= "mature protein"

PN W09856892-A1.
 XX 17-DEC-1998.
 XX 10-JUN-1998; 98WO-US11932.
 XX 11-JUN-1997; 97US-0052991.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Fan P, Gentz RL, Ni J, Yu G;
 DR WPI; 1999-060325/05.
 DR N-PSDB; AAV99927.
 XX New isolated tumour necrosis factor-like receptor, TR9 - used to
 PT develop products for treating e.g. cancers, autoimmune disorders,
 PT viral infections, inflammation, graft rejection, neurodegenerative
 PT disorders or ischaemic injury
 XX Claim 1; Fig 1; 134pp; English.

CC This is the amino acid sequence of the human tumour necrosis factor
 CC receptor (TNFR), TR9 receptor, used in the method of the invention
 CC to develop products to treat disorders such as cancers. The novel
 CC TNFR, TR9, can be used to identify agents for modifying apoptosis.
 CC Agonists can be used to treat diseases associated with increased
 CC cell survival, or the inhibition of apoptosis, including cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, and
 CC hormone-dependent tumours, such as breast cancer, prostate cancer,
 CC Kaposi's sarcoma and ovarian cancer), autoimmune disorders (e.g.
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC rheumatoid arthritis), viral infections (e.g. herpes viruses, pox
 CC viruses and adenoviruses), inflammation, graft vs host disease,
 CC acute graft rejection and chronic graft rejection. Antagonists
 CC can be used to treat diseases associated with increased apoptosis
 CC including AIDS, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC retinitis pigmentosa, cerebellar degeneration), myelodysplastic
 CC syndromes (e.g. aplastic anemia), ischemic injury (e.g. that
 CC caused by myocardial infarction, stroke and reperfusion injury),
 CC toxin-induced liver disease (e.g. that caused by alcohol), septic
 CC shock, cachexia, anorexia, inflammatory diseases and stress response

CC related diseases, such as inflammatory bowel disease, rheumatoid
 CC arthritis, osteoarthritis, psoriasis and septicemia. The products
 CC can also be used for detection and diagnosis.
 XX Sequence 655 AA;
 SQ Query Match 100.0%; Score 3456; DB 20; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGTSPSSSTALACSRITARRATATMIAGSLLLGLFLSTTTTAQPEKQKASNLIGIYRHVDRA 60
 Db 1 MGTSPSSSTALACSRITARRATATMIAGSLLLGLFLSTTTTAQPEKQKASNLIGIYRHVDRA 60
 Qy 61 TGOVLTCDCPKAGTYVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSOPCPWPMEIK 120
 Db 61 TGOVLTCDCPKAGTYVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSOPCPWPMEIK 120
 Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGWGRKKGTTETEDVRCQCARGTFSQV 180
 Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGWGRKKGTTETEDVRCQCARGTFSQV 180
 Qy 181 SSVNCKKAYTDCLSQNLVWIKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPRPHEMTH 240
 Db 181 SSVNCKKAYTDCLSQNLVWIKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPRPHEMTH 240
 Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVDPNTSSARGKEDVNTKLPNLQVNVH 300
 Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVDPNTSSARGKEDVNTKLPNLQVNVH 300
 Qy 301 QQGPVHRLKLLPSMEATGEEKSSTPIKGPGRHPRQNLHKHFDINEHLPMVIVLFL 360
 Db 301 QQGPVHRLKLLPSMEATGEEKSSTPIKGPGRHPRQNLHKHFDINEHLPMVIVLFL 360
 Qy 361 VLVVIVVCSIRKSSRTLLKGRQDPSAIVEKAGLKKSWPTQNKREKWIYCNHGHGIDILK 420
 Db 361 VLVVIVVCSIRKSSRTLLKGRQDPSAIVEKAGLKKSWPTQNKREKWIYCNHGHGIDILK 420
 Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTAHERAYAAHQHTVIRGPEASLAQLIS 480
 Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTAHERAYAAHQHTVIRGPEASLAQLIS 480
 Qy 481 ALRQHRNDVVVEKIRGLMEDTTLQETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 Db 481 ALRQHRNDVVVEKIRGLMEDTTLQETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 Qy 541 SPQDKNGFFVDESEPLRLCDSTSSGSSALSRSNGSFITKEKQTVLRQVRLDPCDLQPIF 600
 Db 541 SPQDKNGFFVDESEPLRLCDSTSSGSSALSRSNGSFITKEKQTVLRQVRLDPCDLQPIF 600
 Qy 601 DDMHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSYSHLPDLL 655
 Db 601 DDMHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSYSHLPDLL 655
 RESULT 3
 AAB26981
 ID AAB26981 standard; Protein: 655 AA.
 XX AAB26981;
 AC AAB26981;
 DT 02-FEB-2001 (first entry)
 DE Human tumour necrosis factor receptor TR9.
 XX Human; tumour necrosis factor; TR9 receptor; immunosuppressive;
 KW antiinflammatory; cardiant; antidiabetic; antidiabetic; antiallergic;
 KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
 KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
 KW common variable immunodeficiency; X-linked agammaglobulinaemia;
 KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
 KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
 KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;

cardiovascular disease; neurological disease; protein coordinate data.

Homo sapiens.

WO2000556862-A1.

28-SEP-2000.

16-MAR-2000; 2000WO-US06831.

24-MAR-1999; 99US-0126019.

14-MAY-1999; 99US-0134220.

(HUMA-) HUMAN GENOME SCI INC.

NI J, Gentz RL, Yu G, Fan P;

WPI; 2000-594575/56.

N-PSDB; AAA99638.

Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy and cancer -

Claim 20; Fig 1; 220pp; English.

The present sequence is a novel human tumor necrosis factor receptor, designated TR9. The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for treating, preventing or diagnosing common variable immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and other neurological diseases.

Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;

Best Local Similarity 100.0%; Pred. No. 6.8e-274;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATMTAGSLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60

DB 1 MGTSPSSSTALASCSRIARRATATMTAGSLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60

QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120

DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120

QY 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPGVGWVKKGTETEDVRCKQCARGTFSQVDP 180

DB 121 LPCAALTDRECTCPGCMFOSNATCAPHTVCPGVGWVKKGTETEDVRCKQCARGTFSQVDP 180

QY 181 SSVMKCKAYTDCLSQNLVVIKPTKETDNVCGTLPFSFSSSTSPSGTATFPRPEHMETHE 240

DB 181 SSVMKCKAYTDCLSQNLVVIKPTKETDNVCGTLPFSFSSSTSPSGTATFPRPEHMETHE 240

QY 241 VPSSTVYPKGMSTENSSASVRPKVLSIQGTVDPDNTSSARGEDVKNKTLPNLQVNVH 300

DB 241 VPSSTVYPKGMSTENSSASVRPKVLSIQGTVDPDNTSSARGEDVKNKTLPNLQVNVH 300

QY 301 QGPHHRHLKLLPSMEATGGKSTPIKGRKGRHPRQNLKHFDINEHLPWMLVFLLL 360

DB 301 QGPHHRHLKLLPSMEATGGKSTPIKGRKGRHPRQNLKHFDINEHLPWMLVFLLL 360

QY 361 VLWVIVVCSIRKSSRTLKGRQDPSAIVEKAGLKKSMPTQTNREKWIYYCNGHGDILK 420

DB 361 VLWVIVVCSIRKSSRTLKGRQDPSAIVEKAGLKKSMPTQTNREKWIYYCNGHGDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGNTADHERAYAAQLQHTWIRGPEASLAQLIS 480

Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGNTADHERAYAAQLQHTWIRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPNAKLENSALLTVEP 540

Db 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPNAKLENSALLTVEP 540

QY 541 SPQDKNKGFFVDESEPLLRCDSTSSGSSALSRRNGSFITTEKKKDTVLRQVRLDPCDLQPIF 600

Db 541 SPQDKNKGFFVDESEPLLRCDSTSSGSSALSRRNGSFITTEKKKDTVLRQVRLDPCDLQPIF 600

QY 601 DDLHFLNPEELRVIEEIPQAEKLDRLFEIIGVKSQEAQSOTLLDSVYSHLPDLL 655

Db 601 DDLHFLNPEELRVIEEIPQAEKLDRLFEIIGVKSQEAQSOTLLDSVYSHLPDLL 655

RESULT 4

AAB01349

ID AAB01349 standard; Protein; 655 AA.

XX

AC AAB01349;

XX

DT 20-OCT-2000 (first entry)

XX

DE Tumour necrosis factor receptor homologue TRH1 (Clone 2733717).

XX

KW Tumour necrosis factor receptor homologue; TRH1; TNF; arthritis;

KW transplant rejection; activation; proliferation; differentiation;

KW apoptosis; immunosuppression; antiinflammatory; immunostimulation;

KW probe; primer; human.

XX

OS Homo sapiens.

XX

PN WO200034294-A2.

XX

PD 15-JUN-2000.

XX

PF 10-DEC-1999; 99WO-US29400.

XX

PR 11-DEC-1998; 98US-0111826.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Bowen MA, Siemers N;

XX

DR WPI; 2000-423364/36.

XX

N-PSDB; AAA47395.

XX

Novel tumor necrosis factor receptor homologue-1 useful as a target for immunosuppressive, antiinflammatory and/or immunostimulatory drug development

PS

Claim 10; Fig 2a-2d; 42pp; English.

XX

The tumour necrosis factor receptor homologue TRH1 can be used for treating a mammal e.g. a human, at risk for a disorder characterized by an aberrant or unwanted level or biological activity of TRH1, e.g. rheumatoid arthritis and transplant rejection. TRH1 may also be useful to leach out or block a ligand which is found to bind to the TRH1. TRH1 may be used in various drug screening techniques and to identify fragments and analogs of a protein or peptide (agonist or antagonist) which bind to TRH1. The TRH1 protein plays a role in cellular function, cell activation, proliferation, differentiation, and apoptosis. The interaction between the novel TRH1 protein of the present invention and intracellular signaling molecules and/or its potential co-receptor may serve as a novel target for immunosuppressive, antiinflammatory and/or immunostimulatory drug development. Gene constructs can also be used as part of a gene therapy protocol to deliver nucleic acids encoding the TRH1, or an agonist or antagonist form of a TRH1 protein or peptide. Antibody directed against TRH1 can be used to reject TRH1 in tissues and cells. They can also be used to make targeted antibody that destroy TRH1 expressing cells. Fragments of the TRH1 gene can be used as diagnostic probes or as PCR primers. Fragments of the full

CC length gene may be used as hybridization probes for a cDNA library to
 CC isolate the full length gene and to isolate other genes which have a
 CC high sequence similarity. The probes may be used to identify a cDNA
 CC clone corresponding to a full length transcript and a genomic clone
 CC or clones that contain the complete gene including regulatory and
 CC promoter regions, exons, and introns.
 XX
 SQ Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
 DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
 QY 61 TQVLTCDKCPAGTVVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMTIEK 120
 DB 61 TQVLTCDKCPAGTVVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMTIEK 120
 QY 121 LPCAALTIRECTCPGPFQSNATCAPHTVCPVGVGRKKGTTEDVRCQKARGTFSDVP 180
 DB 121 LPCAALTIRECTCPGPFQSNATCAPHTVCPVGVGRKKGTTEDVRCQKARGTFSDVP 180
 QY 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 DB 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVKNKTLPLNQVNVH 300
 DB 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVKNKTLPLNQVNVH 300
 QY 301 QOGPHRHRLKLLPSMEATGGKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMIYLFLL 360
 DB 301 QOGPHRHRLKLLPSMEATGGKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMIYLFLL 360
 QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSPAIVEKAGLKKSMPTQNRKWIYCYNGHGDILK 420
 DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSPAIVEKAGLKKSMPTQNRKWIYCYNGHGDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPISPNAKLENSALLTVEP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPISPNAKLENSALLTVEP 540
 QY 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKDDTVLRQVRLDPCDLQPIF 600
 DB 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKDDTVLRQVRLDPCDLQPIF 600
 QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQSLLSVYSHLPDLL 655
 DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEAQSLLSVYSHLPDLL 655

RESULT 5

ID AAB01338
 AC AAB01338 standard; Protein; 655 AA.
 AC AAB01338;
 DT 25-SEP-2000 (first entry)
 DE DR-6 death receptor.
 KW UL144; death receptor; apoptosis; programmed cell death; FAS;
 KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
 KW human.
 OS Homo sapiens.

XX WO200034335-A2.
 PN 15-JUN-2000.
 PD 03-DEC-1999; 99WO-US26035.
 PF 04-DEC-1998; 98US-0205018.
 PR (SCHE) SCHERING CORP.
 XX Leong C, Phillips JH;
 PI WPI; 2000-423383/36.
 DR Purified or recombinant polypeptide for modulating apoptosis comprises
 PT a sequence which binds to an antibody specific for ULI44 or its
 PT fragments
 XX Disclosure; Page 68-70; 76pp; English.
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody
 CC specific for the mature ULI44 is useful for screening molecules which
 CC block induction of apoptosis or interfere with antiapoptotic activity.
 CC The polypeptide is also useful for modulating apoptosis and useful in
 CC treatment of conditions associated with abnormal physiology or
 CC development, such as cancer or degenerative conditions and for
 CC regulation of viral infection and replication. At least five
 CC different death receptors are known, which include the CD95
 CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
 XX SQ Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
 DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLICTYRHVDRA 60
 QY 61 TQVLTCDKCPAGTVVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMTIEK 120
 DB 61 TQVLTCDKCPAGTVVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQPCPWPMTIEK 120
 QY 121 LPCAALTIRECTCPGPFQSNATCAPHTVCPVGVGRKKGTTEDVRCQKARGTFSDVP 180
 DB 121 LPCAALTIRECTCPGPFQSNATCAPHTVCPVGVGRKKGTTEDVRCQKARGTFSDVP 180
 QY 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 DB 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSGTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVKNKTLPLNQVNVH 300
 DB 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVKNKTLPLNQVNVH 300
 QY 301 QOGPHRHRLKLLPSMEATGGKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMIYLFLL 360
 DB 301 QOGPHRHRLKLLPSMEATGGKSSPTIKGPKRGHPRQNLHKHFDINEHLPWMIYLFLL 360
 QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSPAIVEKAGLKKSMPTQNRKWIYCYNGHGDILK 420
 DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSPAIVEKAGLKKSMPTQNRKWIYCYNGHGDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPASLAQLIS 480
 DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNGYTADHERAYAAALQHWITIRGPASLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPISPNAKLENSALLTVEP 540
 DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSFPLSPSPISPNAKLENSALLTVEP 540

Db 481 ALRQHRNDVVEKIRGLMEDTQLETDKALPMPSPSPSPSPNAKLENSALLTVEP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSGSSALSRNGSFITKEKDDTVLRQVRDPCDLOPIF 600
 Db 541 SPQDNKNGFFVDESEPLLRCDSTSGSSALSRNGSFITKEKDDTVLRQVRDPCDLOPIF 600
 QY 601 DDMHLFNPBELRVIEEIPQAEKDLRLFEIIGVKSQASOTLLDSVYSHLPDLL 655
 Db 601 DDMHLFNPBELRVIEEIPQAEKDLRLFEIIGVKSQASOTLLDSVYSHLPDLL 655

RESULT 6
 AAY77460
 ID AAY77460 standard; Protein: 655 AA.
 XX
 AC AAY77460;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Human TNF receptor-like protein HSLJD37R, SEQ ID NO:10.
 XX
 KW TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;
 KW Rank-like protein; RANKL; immune disorder; inflammation; allergy;
 KW immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory;
 KW dermatological; antithyroid.
 XX
 OS Homo sapiens.
 XX
 PN WO200001817-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 06-JUL-1999; 99WO-US12366.
 XX
 PR 06-JUL-1998; 98US-0110938.
 PR 13-JUL-1998; 98US-0114466.
 PR 23-JUL-1998; 98US-0093897.
 PR 12-AUG-1998; 98US-0132968.
 PR 18-AUG-1998; 98US-0136214.
 PR 11-SEP-1998; 98US-0099999.
 XX
 (SCHE) SCHERING CORP.

XX Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
 PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
 PI Bazan JF, Mahony D, Lees EM;
 XX
 DR WPI: 2000-171015/15.
 XX N-PSDB; AA292406.

XX New isolated mammalian genes, used to develop products for treating
 PT e.g. immune, inflammatory or allergic abnormalities, cancers or
 PT degenerative conditions

XX Claim 24; Page 163-165; 218pp; English.

XX The invention relates to a number of primate and/or rodent proteins, and
 CC the genes which encode them. The invention encompasses human dendritic
 CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis
 CC factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL;
 CC human CC chemokine HCC5; human deubiquitinating proteins DUB1 and DUB
 CC 12; human MD-1 and human and murine MD-2 proteins, which exhibit the
 CC properties of ligands for proteins comprising a leucine-rich motif
 CC (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies
 CC against these proteins. The proteins can be used for modulating the
 CC physiology or development of a cell. They can be used to mediate uptake
 CC of substrates (e.g., prostaglandin-like molecules), to modulate or
 CC mediate cellular interactions (e.g., induce or prevent trafficking,
 CC proliferation, or differentiation of cells), or are intracellular
 CC proteins which are important in various cellular processes such as the
 CC deubiquitination of proteins or cell cycle regulation. The products can
 CC be used for treating medical conditions such as immune, inflammatory or
 CC allergic disorders, or abnormal cellular proliferation, for example,

CC cancers or degenerative conditions. They can be used to modulate immune
 CC responses in disease states e.g., autoimmune disorders, including
 CC rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
 CC autoimmune thyroiditis, as well as acute and chronic inflammatory
 CC responses in which T cell activation, expansion, and/or immunological T
 CC cell memory play an important role. Sequences AAY77458-Y77461 and
 CC AAY77465-Y77468 represent TNF receptor family-related proteins. AAY77458
 CC is the human protein HDTEA84, AAY77459-Y77461 are human HSLJD37R
 CC proteins, AAY77465 is murine Rank-like protein RANKL, and AAY77466-Y77468
 CC are human RANKL proteins.

XX SQ Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 21; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
 Db 1 MGTSPPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
 QY 61 TGOVLTCDKCPAGTYVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSQCPWPMEIK 120
 Db 61 TGOVLTCDKCPAGTYVSEHCTNLSRVCSGPCVGTFRHENGIEKCHDCSQCPWPMEIK 120
 QY 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGWGVKKGTEDEVRCKOCARCTFSDVP 180
 Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCPVGWGVKKGTEDEVRCKOCARCTFSDVP 180
 QY 181 SSVNKKAYTDCLSQNLVWIKPGTKETDNNVCGTLPFSSTSSPSGTAIFPRPEHMETHE 240
 Db 181 SSVNKKAYTDCLSQNLVWIKPGTKETDNNVCGTLPFSSTSSPSGTAIFPRPEHMETHE 240
 QY 241 VPSSTYVPKGMNSTESNSSASVVRPKVLSSTOEGTVPDNTSSARCKEDVNTLPLQVYVNH 300
 Db 241 VPSSTYVPKGMNSTESNSSASVVRPKVLSSTOEGTVPDNTSSARCKEDVNTLPLQVYVNH 300
 QY 301 QQGPHHRHILKLLPSMEATGGEKSSSTPIKGPKRGHPRQNLKHFDINEHLPMWLVFLLL 360
 Db 301 QQGPHHRHILKLLPSMEATGGEKSSSTPIKGPKRGHPRQNLKHFDINEHLPMWLVFLLL 360
 QY 361 VLVVVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHIDILK 420
 Db 361 VLVVVVCSIRKSSRTLKGPQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHIDILK 420
 QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNGYTAADHERAVALQHTWIRGPESLAQLIS 480
 Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNGYTAADHERAVALQHTWIRGPESLAQLIS 480
 QY 481 ALRQHRNDVVEKIRGLMEDTQLETDKALPMPSPSPSPSPNAKLENSALLTVEP 540
 Db 481 ALRQHRNDVVEKIRGLMEDTQLETDKALPMPSPSPSPSPNAKLENSALLTVEP 540
 QY 541 SPQDNKNGFFVDESEPLLRCDSTSGSSALSRNGSFITKEKDDTVLRQVRDPCDLOPIF 600
 Db 541 SPQDNKNGFFVDESEPLLRCDSTSGSSALSRNGSFITKEKDDTVLRQVRDPCDLOPIF 600
 QY 601 DDMHLFNPBELRVIEEIPQAEKDLRLFEIIGVKSQASOTLLDSVYSHLPDLL 655
 Db 601 DDMHLFNPBELRVIEEIPQAEKDLRLFEIIGVKSQASOTLLDSVYSHLPDLL 655

RESULT 7
 AAU29232

ID AAU29232 standard; Protein: 655 AA.

XX AAU29232;

AC AAU29232;
 XX
 DT 18-DEC-2001 (first entry)

XX Human PRO polypeptide sequence #209.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW: dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 OS
 XX Homo sapiens.

PN WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.

PR 28-MAR-2000; 2000US-192655P.

PR 29-MAR-2000; 2000US-193032P.

PR 29-MAR-2000; 2000US-193053P.

PR 30-MAR-2000; 2000WO-US0843P.

PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.

PR 11-APR-2000; 2000US-195975P.

PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.

PR 11-APR-2000; 2000US-196690P.

PR 11-APR-2000; 2000US-196820P.

PR 18-APR-2000; 2000US-198121P.

PR 18-APR-2000; 2000US-198585P.

PR 25-APR-2000; 2000US-199397P.

PR 25-APR-2000; 2000US-199550P.

PR 25-APR-2000; 2000US-199654P.

PR 03-MAY-2000; 2000US-201516P.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 05-JUN-2000; 2000US-209832P.

PR 28-JUL-2000; 2000WO-US20710.

CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders.
 XX
 SQ Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 22; Length 655;
 Best Local Similarity 100.0%; Pred. No. 6.8e-274;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPEKASNLGTYRHVDRA 60
 Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPEKASNLGTYRHVDRA 60
 Qy 61 TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFRHENGIEKCHDCSQCPWPMEK 120
 Db 61 TGOVLTCDCPKAGTYVSEHCNTSLRVCSGPCVGTFRHENGIEKCHDCSQCPWPMEK 120
 Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTETEDVRCCKCARGTFSVP 180
 Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTETEDVRCCKCARGTFSVP 180
 Qy 181 SSVMKCKAYTDCLSONLVVVKPGTKETDNVCGTLPSSSSSTSPSGTAIFRPEHMETHE 240
 Db 181 SSVMKCKAYTDCLSONLVVVKPGTKETDNVCGTLPSSSSSTSPSGTAIFRPEHMETHE 240
 Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARKEDVNTKLPNLOVNNH 300
 Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSSIOEGTVPDNTSSARKEDVNTKLPNLOVNNH 300
 Qy 301 QOGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHFDINSHLPMVILFLL 360
 Db 301 QOGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRQNLKHFDINSHLPMVILFLL 360
 Qy 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKMTPTQNKREKVIYCNHGHIDILK 420
 Db 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKMTPTQNKREKVIYCNHGHIDILK 420
 Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHTIRGPEASLAQLIS 480
 Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHTIRGPEASLAQLIS 480
 Qy 481 ALRQRRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 Db 481 ALRQRRNDVVEKIRGLMEDTTQLETDKALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
 Qy 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKTVDVLRVROVRLDPCDLQIF 600
 Db 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRNGSFITKEKKTVDVLRVROVRLDPCDLQIF 600
 Qy 601 DDLHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVSHLPDLL 655
 Db 601 DDLHLFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVSHLPDLL 655

RESULT 8

AAE21958

XX AAE21958 standard; Protein; 655 AA.

XX AAE21958;

XX 25-JUL-2002 (first entry)

XX Human death domain containing receptor (DR6) protein.

XX Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
 KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;

KW: dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 OS
 XX Homo sapiens.

PN WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.

PR 28-MAR-2000; 2000US-192655P.

PR 29-MAR-2000; 2000US-193032P.

PR 29-MAR-2000; 2000US-193053P.

PR 30-MAR-2000; 2000WO-US0843P.

PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.

PR 11-APR-2000; 2000US-195975P.

PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.

PR 11-APR-2000; 2000US-196690P.

PR 11-APR-2000; 2000US-196820P.

PR 18-APR-2000; 2000US-198121P.

PR 18-APR-2000; 2000US-198585P.

PR 25-APR-2000; 2000US-199397P.

PR 25-APR-2000; 2000US-199550P.

PR 25-APR-2000; 2000US-199654P.

PR 03-MAY-2000; 2000US-201516P.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 05-JUN-2000; 2000US-209832P.

PR 28-JUL-2000; 2000WO-US20710.

KW: dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 OS
 XX Homo sapiens.

PN WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.

PR 28-MAR-2000; 2000US-192655P.

PR 29-MAR-2000; 2000US-193032P.

PR 29-MAR-2000; 2000US-193053P.

PR 30-MAR-2000; 2000WO-US0843P.

PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.

PR 11-APR-2000; 2000US-195975P.

PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.

PR 11-APR-2000; 2000US-196690P.

PR 11-APR-2000; 2000US-196820P.

PR 18-APR-2000; 2000US-198121P.

PR 18-APR-2000; 2000US-198585P.

PR 25-APR-2000; 2000US-199397P.

PR 25-APR-2000; 2000US-199550P.

PR 25-APR-2000; 2000US-199654P.

PR 03-MAY-2000; 2000US-201516P.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 05-JUN-2000; 2000US-209832P.

PR 28-JUL-2000; 2000WO-US20710.

KW: dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 OS
 XX Homo sapiens.

PN WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.

PR 28-MAR-2000; 2000US-192655P.

PR 29-MAR-2000; 2000US-193032P.

PR 29-MAR-2000; 2000US-193053P.

PR 30-MAR-2000; 2000WO-US0843P.

PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.

PR 11-APR-2000; 2000US-195975P.

PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.

PR 11-APR-2000; 2000US-196690P.

PR 11-APR-2000; 2000US-196820P.

PR 18-APR-2000; 2000US-198121P.

PR 18-APR-2000; 2000US-198585P.

PR 25-APR-2000; 2000US-199397P.

PR 25-APR-2000; 2000US-199550P.

PR 25-APR-2000; 2000US-199654P.

PR 03-MAY-2000; 2000US-201516P.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 05-JUN-2000; 2000US-209832P.

PR 28-JUL-2000; 2000WO-US20710.

KW: dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 OS
 XX Homo sapiens.

PN WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis; autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic; H. pylori-associated ulceration; anti-inflammatory; vasotropic; virucide; acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective; adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic; dermatological; hepatotropic; antibacterial.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..41
Protein /label= Signal_peptide
41..655
Domain /note= "Mature human DR6"
39..76
Domain /note= "TNFR cysteine rich domain"
77..118
Domain /note= "TNFR cysteine rich domain"
119..162
Domain /note= "TNFR cysteine rich domain"
163..201
Domain /note= "TNFR cysteine rich domain"
339..351
Domain /note= "Transmembrane domain"
360..370
Domain /note= "Transmembrane domain"

WO200185209-A2.

15-NOV-2001.

30-APR-2001; 2001WO-US11735.

10-MAY-2000; 2000US-203015P.

(ELIL) LILLY & CO ELI.

Heuer JG, Liu J, Na S, Song HY, Yang D;

WPI: 2002-351283/38.

N-PSDB; AAD35053.

Treating or preventing T cell or Th2 cell mediated condition e.g., asthma or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist or antagonist -

Claim 11; Page 126-129; 133pp; English.

The invention relates to a method for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. The method comprising administering to the mammal a pharmaceutical composition comprising a death domain containing receptor (DR6) agonist or antagonist. The method is useful for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing lung disease, organ rejection after transplantation, thrombotic thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS) or a condition or symptom related to the above mentioned diseases in a mammal. An DR6 antagonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with immunodeficiency, aberrant apoptosis, bacterial, viral or microbial

infection, complications of infection, human immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori associated ulceration, cytoprotection during cancer treatment, therapy, recuperation from chemotherapy, recuperation from irradiation, or a condition or symptom related to the above mentioned diseases in a mammal. The present sequence is human DR6 protein.

Sequence 655 AA;

Query Match 100.0%; Score 3456; DB 23; Length 655;
Best Local Similarity 100.0%; Pred. No. 6.8e-274;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFSTTTAQPEQKASNLCTYRHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFSTTTAQPEQKASNLCTYRHVDRA 60
QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQPCWPWMIK 120
DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGPCVGTFRHENGIEKCHDCSQPCWPWMIK 120
QY 121 LPCAALTDRCTCPGCMFOSNATCAPHTVCPVGVGWVKKGTETEDVRCQCARGTFSVP 180
DB 121 LPCAALTDRCTCPGCMFOSNATCAPHTVCPVGVGWVKKGTETEDVRCQCARGTFSVP 180
QY 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPCTATFPRPEHMETHE 240
DB 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPCTATFPRPEHMETHE 240
QY 241 VPSSTYVPGKMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLNQLQVNH 300
DB 241 VPSSTYVPGKMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLNQLQVNH 300
QY 301 QOGPHRHILKLLPSWEATGGEKSTTPKGRGRHPRQNLHFKHFDINEHLPWIVLFLLL 360
DB 301 QOGPHRHILKLLPSWEATGGEKSTTPKGRGRHPRQNLHFKHFDINEHLPWIVLFLLL 360
QY 361 VLVWIVVCSIRKSRRTLLKGPQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHGIDILK 420
DB 361 VLVWIVVCSIRKSRRTLLKGPQDPSAIVEKAGLKKSMPTQNRKWIYCNHGHGIDILK 420
QY 421 LVAAQVGSQWKDIYQFLCNASEREVAFAFNGYTAHERAYAAALQHWITRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAFAFNGYTAHERAYAAALQHWITRGPEASLAQLIS 480
QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSPSP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPSPSPSPSPSPSPSPSPSP 540
QY 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSNGSFITKEKKDTVLVRLQVRLDPCDLQPIF 600
DB 541 SPQDNKGFVDESEPLLRCDSTSSGSSALSNGSFITKEKKDTVLVRLQVRLDPCDLQPIF 600
QY 601 DDMLHFLNPEELRVEETIQAEDKLDRLFEIIGVKVSQEAASQTLDSVSHLPDLL 655
DB 601 DDMLHFLNPEELRVEETIQAEDKLDRLFEIIGVKVSQEAASQTLDSVSHLPDLL 655

RESULT 9

AA92846

ID AAY92846 standard; Protein; 691 AA.

XX AC AAY92846;

XX DT 29-AUG-2000 (first entry)

XX DE Human osteoprotegrin-like 4 (OPGx4) protein.

XX KW OPGx4; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;

KW inhibitor; bone resorption; vascular calcification; apoptosis;

KW osteopathic.

[illegible]

AC AAW75792;

```
Db 61 TGOVLTCDKCPAGTYVSEHCNTNTSLRVCSSCPVGTFFRHENGIEKCHDCSQCPWPMTIEK 120
Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Qy 181 SSVMKCKAYTDCLSQNLVWIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFRPRHEMETHE 240
Db 181 SSVMKCKAYTDCLSQNLVWIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFRPRHEMETHE 240
Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
Qy 301 QOGPHRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Db 301 QOGPHRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Db 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Qy 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Db 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Qy 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLQPIF 600
Db 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLQPIF 600
Qy 601 DDLHLFNLPELRVIEIPQAEKDLRLFEIIGVKSQEAASOTILDSVYSHLPDLL 655
Db 601 DDLHLFNLPELRVIEIPQAEKDLRLFEIIGVKSQEAASOTILDSVYSHLPDLL 655

RESULT 12
AAB93023
ID AAB93023 standard; Protein: 655 AA.
XX
AC AAB93023;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:11787.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
```

```
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 11787; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to a
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 655 AA;
```

```
Query Match 99.7%; Score 3444; DB 22; Length 655;
Best Local Similarity 99.7%; Pred. No. 6.6e-273;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPOKASNLIGTYRHVDRA 60
Db 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLSTTTTAQPOKASNLIGTYRHVDRA 60
Qy 61 TGOVLTCDKCPAGTYVSEHCNTNTSLRVCSSCPVGTFFRHENGIEKCHDCSQCPWPMTIEK 120
Db 61 TGOVLTCDKCPAGTYVSEHCNTNTSLRVCSSCPVGTFFRHENGIEKCHDCSQCPWPMTIEK 120
Qy 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Db 121 LPCAALTDRECTCPGFMFQSNATCAPHTVCVPGVGRKKGTEDEVRCKQCARGTSDVP 180
Qy 181 SSVMKCKAYTDCLSQNLVWIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFRPRHEMETHE 240
Db 181 SSVMKCKAYTDCLSQNLVWIKPGTKETDNVCGTLPFSFSSSTSPSPGTAIFRPRHEMETHE 240
Qy 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
Db 241 VPSSTYVPKGMNSTESNSSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNVH 300
Qy 301 QOGPHRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Db 301 QOGPHRHILKLLPSMEATGCKSSTPIKGPGRGHPRONLKHFDINEHLPWMIIVFLLL 360
Qy 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Db 361 VLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPQNREKWIYYCNGHGIDILK 420
Qy 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Db 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHWITIRGPEASLAQLIS 480
Qy 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Db 481 ALRQHRNDVVEKIRGLMEDTTOLETDKALPMSPLSPSPIPSPNAKLENSALLTVEP 540
Qy 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLQPIF 600
Db 541 SPQDNKGGFFVDESEPLLRCDSTSSGSSALSRSNGSFITKEKKDVTLRQVRLDPCDLQPIF 600
```

Db 541 SPQDKNGFFVDESEPLLRCDSTSSGSSALSRRNGSFITKEKDTVLRLQVRLDPCDLPQIF 600
QY 601 DDLHLFLNPEELRVIEIPOAEDKLDLRFELIIGVKQASQTLDSVYSHLPDLL 655
|||||
Db 601 DDLHLFLNPEELRVIEIPOAEDKLDLRFELIIGVKQASQTLDSVYSHLPDLL 655

RESULT 13
AAV05678
ID AAV05678 standard; Protein; 631 AA.
AC AAV05678;
XX
XX 19-JUL-1999 (first entry)
DT Human full-length tumour necrosis factor receptor ZTNFR-6.
DE
XX ZTNFR-6; tumour necrosis factor receptor-6; human;
KW cell maturation; bone cell regulation.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT Peptide
FT 1..17 /note- "signal peptide"
FT Protein
FT 18..631 /note- "mature protein"
FT Protein
FT 18..188 /note- "a polypeptide comprising this region of the
FT sequence is claimed in Claim 28(b)"
FT Protein
FT 18..325 /note- "a polypeptide comprising this region of the
FT sequence is claimed in Claim 28(c)"
FT Protein
FT 37..188 /note- "a polypeptide comprising this region of the
FT sequence is claimed in Claim 28(a)"
FT Protein
FT 66..145 /note- "a polypeptide comprising this region of the
FT sequence is claimed in Claim 26(a)"
FT Region
FT 37..65 /note- "extracellular, cysteine-rich repeat"
FT Region
FT 66..107 /note- "extracellular, cysteine-rich repeat"
FT Region
FT 108..145 /note- "extracellular, cysteine rich repeat"
FT Region
FT 146..188 /note- "extracellular, cysteine-rich repeat"
FT Region
FT 189..325 /note- "extracellular, cysteine-rich repeat"
FT Region
FT 326..346 /note- "linker region"
FT Domain
FT 347..631 /note- "transmembrane domain"
FT Domain
FT 390..471 /note- "cytoplasmic domain"
FT Domain
FT /note- "death domain, specifically claimed in
FT Claim 32(a)"
XX WO9911790-A1.
PN
XX
XX 11-MAR-1999.
XX 98NO-US18364.
PF 03-SEP-1997;
PR 97US-0923725.
PR 04-SEP-1997;
XX 97US-0057608.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Farrah TM, Gross JA, Matthews SM;
PI WPI; 1999-205190/17.
DR N-PSDB; AAX25259.
DR
XX

PT New secreted or membrane bound tumor necrosis factor receptor
XX ZTNFR-6 - useful for detecting a genetic abnormality in a patient
PS Claim 26; Page 113-115; 145pp; English.
XX
CC The present sequence represents a novel human full-length
CC membrane-bound tumour necrosis factor receptor, designated ZTNFR-6,
CC that is characterised by 4 cysteine-rich pseudo-repeat motifs.
CC ZTNFR-6 polypeptides can be obtained using recombinant techniques.
CC A polynucleotide (see AAX25259) encoding ZTNFR-6 has been isolated
CC from an EST database. A secreted, soluble form (see AAY05679) of
CC ZTNFR-6 has also been identified, which lacks the transmembrane
CC and cytoplasmic domains of the membrane-bound protein. ZTNFR-6
CC polypeptides, including the isolated extracellular region,
CC transmembrane domain and death domain, are claimed. ZTNFR-6
CC polypeptides are useful in methods that promote cellular maturation
CC and bone cell regulation. Antibodies raised against ZTNFR-6 are
CC useful for immunohistochemical tagging of cells expressing ZTNFR-6
CC for use in diagnosis, isolating ZTNFR-6, generating anti-idiotypic
CC antibodies, and as neutralising antibodies or antagonists that block
CC ZTNFR-6 in vivo and in vitro. The polypeptides can also be used to
CC identify agonists and antagonists of ZTNFR-6. Agonists are useful
CC for modifying the proliferation and development of target cells in
CC vitro and in vivo.
XX
SQ Sequence 631 AA;
Query Match 96.7%; Score 3342; DB 20; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.4e-264; Indels 0; Gaps 0;
Matches 631; Conservative 0; Mismatches 0;
QY 25 MIAGSLLLLGFLSTTTTAQPEQKASNLIGYRHHVDRATGQVLTCDKCPAGTYVSEHCNTIS 84
|||||
DB 1 MIAGSLLLLGFLSTTTTAQPEQKASNLIGYRHHVDRATGQVLTCDKCPAGTYVSEHCNTIS 60
QY 85 LRVCCSCPVTGTRHENGIEKCHDCSQCPWPWIEKLPCAALTDRECTCPPGFMQSNATC 144
|||||
DB 61 LRVCCSCPVTGTRHENGIEKCHDCSQCPWPWIEKLPCAALTDRECTCPPGFMQSNATC 120
QY 145 APTVCVPGVGVKKGKTETEDVRCKOCARGTFSDVPSSVMKCKAYTDCLSQNLVLVTKPT 204
|||||
DB 121 APTVCVPGVGVKKGKTETEDVRCKOCARGTFSDVPSSVMKCKAYTDCLSQNLVLVTKPT 180
QY 205 KETDNYCGTLPSPSSSTSPSGTAIFRPEHMETHEVPSSTYVPKGMNSTESSASVRP 264
|||||
DB 181 KETDNYCGTLPSPSSSTSPSGTAIFRPEHMETHEVPSSTYVPKGMNSTESSASVRP 240
QY 265 KVLSSIQEGTVPDNTSSARGKEDVNTLPNLQVNVHQGPVHRRHILKLLPSMEATGGEKS 324
|||||
DB 241 KVLSSIQEGTVPDNTSSARGKEDVNTLPNLQVNVHQGPVHRRHILKLLPSMEATGGEKS 300
QY 325 STPIKGPKRGHPRQNLKHFIDINEHLPWMIVLFLVLLVIVVVCSTRKSSRTLKKGPROD 384
|||||
DB 301 STPIKGPKRGHPRQNLKHFIDINEHLPWMIVLFLVLLVIVVVCSTRKSSRTLKKGPROD 360
QY 385 PSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASERE 444
|||||
DB 361 PSAIVEKAGLKKSMPTQNRKWIYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASERE 420
QY 445 VAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMETTOL 504
|||||
DB 421 VAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMETTOL 480
QY 505 ETDKALPMSPLSPSPSPNAKLENSALLTVPESPQDKNGKGFVDESEPLLRCDSTS 564
|||||
DB 481 ETDKALPMSPLSPSPSPNAKLENSALLTVPESPQDKNGKGFVDESEPLLRCDSTS 540
QY 565 SGSSALSRNGSFITKEKDTVLRLQVRLDPCDLPQIFDDMLHFLNPEELRVIEIPOAEDK 624
|||||
DB 541 SGSSALSRNGSFITKEKDTVLRLQVRLDPCDLPQIFDDMLHFLNPEELRVIEIPOAEDK 600
QY 625 LDRLEFIIGVKQASQTLDSVYSHLPDLL 655
|||||

601 LDRLEIIGVKQSEASOTLLDSVYSHLPDLL 631

RESULT 14

ID AAE21959 standard; Protein: 631 AA.

AC AAE21959;

DT 25-JUL-2002 (first entry)

DE Human death domain containing receptor (DR6) protein fragment.

Human; therapy; death domain containing receptor; DR6; receptor; anaemia; apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis; diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis; autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic; H. pylori-associated ulceration; anti-inflammatory; vasotropic; virucide; acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective; adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic; dermatological; hepatotropic; antibacterial.

OS Homo sapiens.

XX WO200185209-A2.

XX 15-NOV-2001.

XX 30-APR-2001; 2001WO-US11735.

XX 10-MAY-2000; 2000US-203015P.

XX (ELIL) LILLY & CO ELI.

PI Heuer JG, Liu J, Na S, Song HY, Yang D;

DR WPI; 2002-351283/38.

PT Treating or preventing T cell or Th2 cell mediated condition e.g., asthma or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist or antagonist.

XX Example 11; Page 129-131; 133pp; English.

The invention relates to a method for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. The method comprising administering to the mammal a pharmaceutical composition comprising a death domain containing receptor (DR6) agonist or antagonist. The method is useful for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft-versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's thyroiditis, Graves disease, transplant rejection, systemic lupus erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune infertility, Behcet's disease, autoimmune gastritis, fibrosing lung disease, organ rejection after transplantation, thrombotic thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS) or a condition or symptom related to the above mentioned diseases in a mammal. An DR6 antagonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with immunodeficiency, aberrant apoptosis, bacterial, viral or microbial infection, complications of infection, human immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori

CC associated ulceration, cytoprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, or a condition or symptom related to the above mentioned diseases in a mammal. The present sequence is human DR6 protein fragment.

SQ Sequence 631 AA;

Query Match 96.7%; Score 3342; DB 23; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.4e-264;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	25	MIAGSLLLGLSTTTTAQPEKASNLIGTRHVDVDRATQVLTCDKCPAGIYVSHCNTS	84
Db	1	MIAGSLLLGLSTTTTAQPEKASNLIGTRHVDVDRATQVLTCDKCPAGIYVSHCNTS	60
Qy	85	LRVSSCPVGTFTTHENGIEKCHDCSOPCPWPMIEKLPCALTDRECTCPGMEQSNATC	144
Db	61	LRVSSCPVGTFTTHENGIEKCHDCSOPCPWPMIEKLPCALTDRECTCPGMEQSNATC	120
Qy	145	APHTVCPVGVGRKKGTETEDVRCKQCARGTFSDVSSVMKCKAYTDCLSQNLVIRPGT	204
Db	121	APHTVCPVGVGRKKGTETEDVRCKQCARGTFSDVSSVMKCKAYTDCLSQNLVIRPGT	180
Qy	205	KETDNVCGTLPSSSSTSPSPGTAIFRPERHMETHEVPSSTIYVPGKMNSTESNASVVP	264
Db	181	KETDNVCGTLPSSSSTSPSPGTAIFRPERHMETHEVPSSTIYVPGKMNSTESNASVVP	240
Qy	265	KVLSSIOEGTVPDNTSSARGKEDVNTLPNLQVNVHQQGPHRHILKLLPSMEATGGEKS	324
Db	241	KVLSSIOEGTVPDNTSSARGKEDVNTLPNLQVNVHQQGPHRHILKLLPSMEATGGEKS	300
Qy	325	STPIKPKRGHPRQNLHKHFDINEHLPWMIVFLFLLLVLVIVVCSIRKSSRTLKKGPRQD	384
Db	301	STPIKPKRGHPRQNLHKHFDINEHLPWMIVFLFLLLVLVIVVCSIRKSSRTLKKGPRQD	360
Qy	385	PSAIVERAGLKKSWPTQNKREKWIYCNHGHIDILKLVAAQVGSQWKDIYQFLCNASERE	444
Db	361	PSAIVERAGLKKSWPTQNKREKWIYCNHGHIDILKLVAAQVGSQWKDIYQFLCNASERE	420
Qy	445	VAAFSNGYTADHERAYAAALQHWITRGPEASLAQLISALRQHRNDVYVEKIRGLMEDTTOL	504
Db	421	VAAFSNGYTADHERAYAAALQHWITRGPEASLAQLISALRQHRNDVYVEKIRGLMEDTTOL	480
Qy	505	ETDKLALPMSPLSPSPPIPSNKLNSALLTYVEPQDNKNGFFVDESEPLLRCDSTS	564
Db	481	ETDKLALPMSPLSPSPPIPSNKLNSALLTYVEPQDNKNGFFVDESEPLLRCDSTS	540
Qy	565	SGSSALSRNGSFITKEKKDVTLRQVRLDPCDLQIFDDMLHFLNPEELRVITEEIPQABDK	624
Db	541	SGSSALSRNGSFITKEKKDVTLRQVRLDPCDLQIFDDMLHFLNPEELRVITEEIPQABDK	600
Qy	625	LDRLEIIGVKQSEASOTLLDSVYSHLPDLL 655	
Db	601	LDRLEIIGVKQSEASOTLLDSVYSHLPDLL 631	

RESULT 15

ID AAY05697 standard; Protein: 605 AA.

AC AAY05697;

DT 19-JUL-1999 (first entry)

DE Human TNF receptor TRL II.

XX TRL II; TNF receptor-like; tumour necrosis factor receptor; human; signal transduction; cell differentiation; prostate cancer; inflammation; arthritis; diabetes; insulin resistance; diagnosis; therapy.

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers	
FT	Peptide	1..41	
FT		/note= "signal peptide"	
FT	Protein	42..605	
FT		/note= "mature protein"	
FT	Domain	47..89	
FT		/note= "cysteine-rich domain"	
FT	Domain	90..131	
FT		/note= "cysteine-rich domain"	
FT	Domain	132..169	
FT		/note= "cysteine-rich domain"	
FT	Domain	170..212	
FT		/note= "cysteine-rich domain"	
FT	Domain	352..370	
FT		/note= "transmembrane domain"	
FT	Domain	415..498	
FT		/note= "death domain"	
XX			
PN	W09915663-A1.		
XX			
PD	01-APR-1999.		
XX			
PF	25-SEP-1998;	98WO-US20219.	
XX			
PR	17-MAR-1998;	98US-0042785.	
PR	26-SEP-1997;	97US-0938896.	
XX			
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.		
XX			
PI	Busfield SJ;		
XX			
DR	WPI; 1999-254712/21.		
DR	N-PSDB; AAX25322.		
XX			
PT	Nucleic acid encoding tumor necrosis factor receptor-like protein		
XX			
PS	Claim 1d; Page 154-157; 170pp; English.		
XX			
CC	The present sequence represents human TRL II (TNF receptor-like), a novel member of the tumour necrosis factor receptor superfamily. The sequence is predicted from the sequence of a cDNA clone (see AAX25322) isolated from an HeLa cell cDNA library. TRL II is a 66.2 kDa membrane-bound protein includes 4 cysteine-rich domains and a C-terminal unique region containing a death domain. An alternatively spliced secreted form, human TRL I (see AAY05696), has also been identified. The invention provides full-length TRL proteins, TRL fusion proteins, antigenic peptides and anti-TRL antibodies, as well as TRL nucleic acids, recombinant expression vectors, host cells and non-human transgenic animals. TRLs are regulators or modulators of cellular signal transduction, cellular proliferation or differentiation, cell survival and apoptosis, immune system cells, and cells involved in insulin resistance or the diabetic response. They can be used to isolate cognate ligands, to modulate ligand/TRL interactions, to screen for potential modulators, and to treat conditions associated with abnormal TRL levels. Antibodies, TRL protein mutants etc. that modulate activity of TRL are also used to treat/prevent conditions associated with aberrant TRL protein or expression, e.g. cell proliferation and differentiation disorders (particularly cancer, especially of the prostate), inflammation (e.g. arthritis) and metabolic disease (e.g. diabetes and insulin resistance).		
XX			
SQ	Sequence	605 AA;	
	Query Match	83.7%; Score 2892; DB 20; Length 605;	
	Best Local Similarity	100.0%; Pred. No. 9,1e-228;	
	Matches 544; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MGTSPSSSTALACSRITARRATMTAGSLLLLGLFSTTTAQPPOKASNLIGTVRHVDRA	60
Db	1	MGTSPSSSTALACSRITARRATMTAGSLLLLGLFSTTTAQPPOKASNLIGTVRHVDRA	60
QY	61	TGQVLTCDKCPAGTVYSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSPCPWPMEK	120

Search completed: July 11, 2003, 15:47:46
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:46:53 ; Search time 22 Seconds
(without alignments)
2862.184 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

Sequence: 1 MGTPSSSTALASCRIARR.....SQEASOTLDSVSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2350	68.0	651	2	death receptor-6 -
2	343.5	9.9	461	1	tumor necrosis fac
3	275.5	8.0	459	2	gene murine tumour
4	273.5	7.9	474	2	tumor necrosis fac
5	236.5	6.8	416	1	nerve growth facto
6	235.5	6.8	255	2	lymphocyte activat
7	233	6.7	305	2	B cell-associated
8	228.5	6.6	435	2	tumor necrosis fac
9	218.5	6.3	326	1	T2 protein - myxom
10	211.5	6.1	325	2	nerve growth facto
11	211.5	6.1	425	1	nerve growth facto
12	210.5	6.1	427	1	hypothetical prote
13	206.5	6.0	348	2	gene G4R protein -
14	206.5	6.0	349	2	CD30 antigen precu
15	205	5.9	595	2	G2R protein - vari
16	204.5	5.9	349	2	B-cell activation
17	200	5.8	277	2	tumor necrosis fac
18	193	5.6	461	2	hypothetical prote
19	191.5	5.5	2824	2	membrane glycoprot
20	187.5	5.4	493	2	tumor necrosis fac
21	186.5	5.4	461	1	T-cell antigen 4-1
22	180.5	5.2	256	2	tumor necrosis fac
23	170	4.9	454	1	Ox40 homolog - hum
24	154	4.5	277	2	Ox40 antigen precu
25	148	4.3	271	2	tumor necrosis fac
26	145.5	4.2	455	1	laminin B2 chain
27	142.5	4.1	1193	2	hypothetical prote
28	138	4.0	1827	2	hypothetical prote
29	136.5	3.9	1205	2	hypothetical prote

30	136.5	3.9	1372	2	T25933	hypothetical prote
31	136	3.9	272	2	I48700	gene ox40 protein
32	135.5	3.9	5376	2	T42215	zonadhesin - mouse
33	132.5	3.8	1252	2	S36016	ocyst wall protei
34	129.5	3.7	3570	2	T45025	mucin MUC5B, trach
35	129	3.7	1459	2	T30196	hypothetical prote
36	128.5	3.7	634	2	T00388	mouse developmenta
37	128.5	3.7	987	2	I48652	hypothetical prote
38	128.5	3.7	1032	2	T34433	hypothetical prote
39	128.5	3.7	2232	2	T34434	epn-related recept
40	127.5	3.7	987	2	I48953	lin-15B protein -
41	126	3.6	1440	2	T27942	hepatocyte growth
42	125.5	3.6	1379	1	S01254	variant-specific s
43	123.5	3.6	557	2	A48434	glucan 1,4-alpha-g
44	123.5	3.6	1367	1	S48478	coagulation factor
45	123	3.6	2183	2	T42764	

ALIGNMENTS

RESULT 1

JC7705

Death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: JC7705

R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belo

trates, activates a cell death and/or survival signaling cascade.

C:Genetics:

A:Gene: dr-6

C:Keywords: ovary

F:1-21/Domain: signal sequence #status predicted <STG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DED>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 68.0%; Score 2350; DB 2; Length 651;

Best Local Similarity 70.6%; Pred. No. 1.8e-148;

Matches 469; Conservative 47; Mismatches 102; Indels 46; Gaps 10;

QY 23 ATMTAGSLLGLGFLSTTTAQP-----EOKASNL-IGTYRHVDRTGQVLTCDKCPAGTVVS 77

Db 3 AAVLAALPLVLVLGTDADQPKLTSEQNAVSLPAGKYLHLDRTATNQELCDKCPAGTVVS 62

QY 78 EHCNTSLRVSSGSPVGTFTTHRENGIEKCHDCSPCPWPMIEKLPCCALTDRECTCPGP 137

Db 63 KHCYKSTLRKSPCPDGTFTTHRENGIERCHPCRPCELPMEIKTHTCTALTDRCTCLSGT 122

QY 138 FOSNATCAPHTVCPVGVGRKKGTETEDVRCKQARGTFSDVPSSVMCKKAYTDCLSQNL 197

Db 123 FQINDTCVPYTVCPVGVGRKKGTETEDVRCKPCLRGTFSDVPSSVMCKKTYTDCFGKN 182

QY 198 VVIRPGTKETDNCV---GTLF--SFSSSTSPGTAIFPRHEHMETHEVSPSTVYPKGMN 252

Db 183 VVIRPGTKESDNCVSPASLPNTSLTSSDAQDG-----ETYEAPPTAYLPKGLN 232

QY 253 STENSSASVRPKVLSSIQEGTVPDNTSSARGKEDVKNLTPLNQVNVNQHQPHRHILKL 312

Db 233 SSVFDLSSSPAPRVSYNGTAETVDYNDTSANGTVGAPGSLSSAGTAGOQSYRKHHTSQA 292

QY 313 L---PSMEATGGEKSSPTIKGPKRGHPQNLKHFIDINEHLPWMIVLFLLLVIVVVCVS 369

Db 293 MGKQPAQEMAGGKSSIPYRPRGPP--NVHQHFDINEHLPWMIVLFLLLVIVVVCVS 350

F;TJ1-100/DOMI.II: NO

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A;Residues: 1-22 <KIS>

Matches	Conservative	Mismatches	Indel's	Gaps
82	34	127	85	85

Matches	82;	Conservative	34;	Mismatches	127;	Indel's	85
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Db 53 MCCA KCPPGQYVKHFCNKTS DTVCADCEASMYTQVWNQFRTCLSCSSCTTDQVEIRACT 112

Db 113 KQNRVCACEAGRYCALKTHSGSCRQCQMRSLKCGPGFVASSRAPNGNVLCACAPGTF 172

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0v -----NIQVYN-----HOCGRH-----HBHTTK 311

QY 312 LLPSMEATGGEKSST--PIKGPKRGHPR 337 .

RESULT 5

Nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor

R; Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, Neurosci 2 1123-1134 1980

A;Accession: UN0000
A;Molecule type: mRNA

R/Heuer, J.G.; FACHELLE-NAHNE, S.; WHEELER, E.F.; BOTHWELL, M.
Dev. Biol. 137, 287-304, 1990

A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation

C;Comment: This receptor is found on sensory and sympathetic neurons, on neuro
C;Comment: The cysteine-rich region of the extracellular domain may form part

F;1-20/Domain: signal sequence #status predicted <SIG>

F;59-100/Domain: NGF receptor repeat homology <NG2>

JN0006
nerve arc

N: Alternate names: NGF receptor
C: Species: Gallus gallus (chicken)

C;Accession: JN0006; A60504
B:Large, T.H.: Weskamp, G.: Helder, J.C.: Radeke, M.J.: Misko, T.P.: Shooter

A;Title: Structure and developmental expression of the nerve growth factor A;Reference number: JN0006: MUID:90166579: PMID:2560385

A;Molecule type: mRNA
A;Residues: 1-416 <LAR>

R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990

A;Reference number: A60504; PMID:2154393
A:Accession: A60504

A;Molecule type: mRNA
A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>

C;Comment: The cysteine-rich region of the extracellular domain may form part of a high-affinity receptor when it interacts with the extracellular domain of the other subunit.

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; F.1-20/Domain: signal sequence #status predicted <SIG>

F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NCF receptor repeat homology <NC1>

F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NCA>

F:189-237/Region: serine/threonine-rich
F:240-261/Domain: transmembrane #status predicted <MEM>
F:262-416/Domain: intracellular #status predicted <INT>
F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 236.5; DB 1; Length 416;
Best Local Similarity 23.2%; Pred. No. 3.3e-08;
Matches 105; Conservative 50; Mismatches 191; Indels 107; Gaps 15;

QY 67 CDKCPAGTVVSEHCTNLSLRVSSC-PVGTFTREHNGIEKCHDCSQPCWPMEIKLPCAA 125
DB CRACNLGEGVQPC-CVNGTVCEPCLDSVTYSATVPCKPCTQ-CVGLHSMSPACVE 93
QY 126 LTDRECTCPGPMFQS--NATCAPHTYCPVGVGWRKKGTTEDVRCQCARGFSDVPSSV 183
DB SDDAVCRKAVGYFQDELSSGCRBCSICEVGFGLMFPQRDSQDVTVECEPGEFTSDEANFV 153
QY 184 MKCKAYTDCLSQNLVVIKGTETDNVCGTL-----PSFSSSTSPSPGTAIFRPEH 235
DB DPLCLPTIC-EENEVMKECTATSDAECRLDHPRTWTHTPSLAGSDSPETITRDPTNEG 212
QY 236 METHPEVPSSTYVPKGMNSESNSAS---VRPKVLSIQEGTVDPNTSSARGKEDVNKT 291
DB MATTLADIYTVMGSSQPVSRGTADNLIPVCSILAAVVGVLVAVIAFKRNNSCKONKO 272
QY 292 LPNLQVNVHQCPHRRHILKLLPSMEATGGEKSSTPIKPKRGHPQRNLKHFDINEHLP 351
DB GANNRPVNQTPSP-----GEK-----LHSDSGI----- 296
QY 352 WMIVLELLLVVIVVVCSTIRKSRTLKKGPQDPSAIVK--AGLKKSTPTQNRKWIY 409
DB -----SDVSLHDQPPNOSTQGPAPKGDGSLVSLPPSKQEB----- 335
QY 410 YCNGHGIDILKLVAAQGVGQWDIYQFLCNASEREVAFNSGY-----RADHERAVA 461
DB -----VEKLSSSAETWQQL-----AGELGYKEDLIDCFTEESPARA 374
QY 462 ALQHTWIRGEASLAQLSRHNRNDVVEKI 494

DB 375 LLADWSAK-ETATLDALLVALRKIQGRDIAESL 406

RESULT 6

I38426

Lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38426; J07052

R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; Eur. J. Immunol. 24, 2219-2227, 1994
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
A:Reference number: I38426; MUID:94374434; PMID:8088337

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <RES>

A:Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321

R:Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A:Reference number: J07052; MUID:94085794; PMID:8262389

A:Accession: J07052

A:Molecule type: mRNA

A:Residues: 1-106, 'r', 108-255 <SCH>

C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neuro
C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix
C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>

F:187-213/Domain: transmembrane #status predicted <TM>

F:138, 149/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:234, 235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted

F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
Query Match 6.8%; Score 235.5; DB 2; Length 255;
Best Local Similarity 30.4%; Pred. No. 2.1e-08;
Matches 63; Conservative 24; Mismatches 77; Indels 43; Gaps 8;

QY 25 MIAGSLLLLGFLSTTTTAQPEQKASNLIGTYRHRVDRATGQVLTKCDKCPAGTYVSEHCTNTS 84
DB 8 IVATLLLVLFNFRSLQD-----PCSNCPAGTF-----CDNNR 41
QY 85 LRVCSCTPVGTFTREHNGIEKCHDCSQPCWPMEIKLPAAALTDRECTCPGWFQSNATC 144
DB 42 NQICSPCPNFS-SAGQRTCDICRQ-CKGVFTRKECSSTSNAECDCTPGFHCGLGAGC 99
QY 145 AP-HTVCPVGVGWRKKGTTEDVRCQCARGFSDVPSSVMKCKAYTDCLSQNLVVIKPG 203
DB 100 SMCEQDCKQGOELTKG-----CKDCGFTFNDQKRGII--CRPTWNTSLDGKSLVING 150
QY 204 TKETDNVCGTLPS-----FSSSTSPSP 225
DB 151 TKERDVVCGPSADLSPGASVTPPAP 177

RESULT 7

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur

A:Reference number: A46476; MUID:92105763; PMID:1370315

A:Accession: A46476

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: GB:M83312; NID:gl553058

A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay

J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586; PMID:1281194

A:Accession: A46515

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'LV' <GRI>

A:Cross-references: GB:M83312; NID:gl553058; PIDN:AAB08705.1; PID:gl553059; GB:M94126

A:Experimental source: BALB/c, liver

A:Note: sequence extracted from NCBI backbone (NCBIP:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Comment: For an alternative splice form, see PIR:A46476.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 6.7%; Score 233; DB 2; Length 305;

Best Local Similarity 34.9%; Pred. No. 3.8e-08;

Matches 53; Conservative 21; Mismatches 70; Indels 8; Gaps 4;

QY 67 CDKCPAGTYVSEHCTNLSLRVSSCPVGTFTREHNGIEKCHD---CSQPCPWPMEIKLP 123
DB 38 CDLCQPGSLTSHCTALEKTQCHPCDSGFEQAQWNRIRCHQHRHC-EPNQLRVKK-BG 95
QY 124 ALTDRECTCPGPMFQSN---ATCAPHTVCPVGVGWRKKGTTEDVRCQCARGFSDVP 180
DB 96 TAESDVTVCYCKEQGCHTCKDCEACAQHTPCIFGFGYEMENATETDTVCHPCVPVGFNS 155
QY 181 SSMVKCKAYTDCLSQNLVVIKGTETDNVCG 212
DB 156 SLFEKCYPTWSCDKNLEVLQKGTSTQTNWICG 187

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Db      98 KTRDRVDCSAGNVLLKGEGCRICAPKTKCPAGYGV-SGHTRTGDVLTCKPRTYTSD 156
QY      179 VPSSVMKCKAYTDCLS 194
          || : : : |
Db      157 AVSSTETCTSSFNVIS 172

RESULT 10
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Virolgy 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer
F;64-105/Domain: NGF receptor repeat homology <NG2>
A:Reference number: A43692; MUID:87321103; PMID:2820128
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:CROSS-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>

Query Match      6.1%; Score 211.5; DB 2; Length 325;
Best Local Similarity 36.7%; Pred. No. 1.1e-06;
Matches 47; Conservative 7; Mismatches 67; Indels 7; Gaps 2;

QY      65 LTCDKCPAGYYVEHCNTNLSRVCSGPCVGTFTFRHENGIEKHCHDSCQPSPWPIEKLPKA 124
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      38 LCCASCHPGFYASRLCGSGNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLSSESQPCD 97
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      125 ALTDRECTCPGMF-----QSNATCAPHTVCVPGWGVRKKGTETEDVRCKQCARGTFSD 178
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Db      98 RTHDRVNCSTGNVYLLKGONGCRICAPQTCKPAGYGV-SGHTRAGDTLCEKCPPHTYTSD 156

QY      179 VPSSVMKC 186
          || : : |
Db      157 SLSPTERC 164

RESULT 11
A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115899; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:CROSS-references: GB:Q05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
E:Metsis, M.; Timmusk, T.; Allikmeets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid
A:Reference number: PH1229; MUID:93077038; PMID:1446821
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:CROSS-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
```

F;1-29/Domain: signal sequence #status predicted <SIG>		
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>		
F;30-251/Domain: extracellular #status predicted <EXT>		
F;33-66/Domain: NGF receptor repeat homology <NG1>		
F;68-109/Domain: NGF receptor repeat homology <NG2>		
F;110-148/Domain: NGF receptor repeat homology <NG3>		
F;150-190/Domain: NGF receptor repeat homology <NG4>		
F;198-249/Region: serine/threonine-rich		
F;252-273/Domain: transmembrane #status predicted <MEM>		
F;274-425/Domain: intracellular #status predicted <INT>		
F;61/Binding site: carbohydrate (asn) (covalent) #status predicted		

Query Match	6.1%	Score 211.5;	DB 1;	Length 425;
Best Local Similarity	22.9%	Pred. No. 1.6e-06;		
Matches 119;	Conservative 59;	Mismatches 196;	Indels 145;	Gaps 25;

QY	12	ASCSRIARRATATNIAGSLLLGLFLSTTTAQPEOKASNLICTYRHVDRATQVLTCDKCP	71
DB	6	AACSAMDRL-----RLLLLLTGVSSGSAKETCST--GLYTH----SGE--CCRACN	49
QY	72	AGTVVSEHCNTSLRVCSGPCVG--TFTRHENGIEKCHDCSPCPWPMTKEKLPCCAALTDRE	130
DB	50	LGEVGAQPC--GANQTCVEPCLDNVTFSDVVSATEPCPKPCTE--CLGLASMSAPCPEADAV	107
QY	131	CTCPPGMFQSNAT--CAPHTVCPVGWVRKKGKTETEDVRCKQCARGTFSDVPSSVMKCA	188
DB	108	CRCAYYGYQDEETGHCEACSVCEVSGGLVFSCQDKQNTVCECEPGEVYDEANHVDPCLP	167
QY	189	YTDCLSNLVVVKPGTKETDNVCGTLPSFSSTSPSPGTAIFPRPEHMETHEVPSSTVYP	248
DB	168	CTVC--EDTERQLRECTPWADAECIEPG-----RWIPRST--PP	203
QY	249	KGNNST--ESNSSASVRPKVLSSIQEGVDPNTSSARGKEDVNTKLPNLVNVNHQGGPHR	307
DB	204	EGSDSTAPSTQPEVPEP--QDLVPSTVADMVTVMG-----	238
QY	308	HILKLLPSMEATGGEKSTSIKPKRGHPRONLHKHFEDINEHLPWMIVFLLLVLVTVV	367
DB	239	-----SSQPV--VTRG--TTDNL-----IP--VVCISIAAAVVVGLV	268
QY	368	CSIR-----KSSRTLKKGPRODPSNAIVEKAGLKKSMTPTONREKIYYCNGHGIDILKVA	423
DB	269	AYAFKRWNSCKNKGANSRP-----VNQTPPEGEK--LHSDSGISVDSQSLSHD	317
QY	424	AQVGSOWK-----DIQFLCNASEREVAEFSNGVTADH-----ERAY-----	460
DB	318	QQTHTQTASQALKGDGNLXSSPLTRKEVEEKLINGDTWRHLAGELGYPQEHIDSTFHE	377
QY	461	-----AALQHWITIRGPASLAQLISALRQHRNRDNDVVEKI	494
DB	378	ACPVRALLASWGAAQ--DSATDALLAAURRTORADIVESL	415

A:Molecule type: protein
A:Residues: 23-31,'T','33-42','TT','45-46','TX','50-51','XX','54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: This sequence has been corrected by a note added in proof to follow the nucleotide sequence of the gene.
R:Vissavajhala, P.; Leszyk, J.D.; Lin-Goeke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A>Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
A:Reference number: I57638; MUID:89096903; PMID:2850481
A:Accession: I57638
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associate
C:Comment: This receptor undergoes both N- and O-linked glycosylation.
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:I20234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-28/Domain: signal sequence #status predicted <SIG>
F:23-427/Product: nerve growth factor receptor #status experimental <MAT>
F:23-427/Product: nerve growth factor receptor #status experimental <MAT>
F:23-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 210.5; DB 1; Length 427;
Best Local Similarity 22.8%; Pred. No. 1.8e+06;
Matches 116; Conservative 58; Mismatches 204; Indels 131; Gaps 22;

Qy 21 ATATMTAGSLLLGIFLSTTAQPEOKASNLGTYRHVDRTAQVLTCDKPCAGTVYSEHC 80
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 5 ATGRAMDGPRLILLGLLVSLGGAKBACP-TGLYTH----SGE--CCKACNLGEGVAQPC 57
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 81 TWTSLRVCSGC-PVGTFTRHENGIEKCHDCSPCPWPMIEKLPCALTDRECTCPPGMFQ 139
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 58 -GANQTVCBPCLDSVTSDVWSATEPKPCTE-CVGLQMSAPCEADDAVCRCAIYYQ 115
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 140 SNAT--CAPHTVCPGVGWRRKGTEDEVRCQKARGTESDPSSVMCKAYTDCLSQNL 197
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 116 DETTGRCACRVEAGSLVFSCQDKQNTVCECDPDGYSDANHWDCPLCTVC-EDTE 174
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 198 VIKPTKETDNVC-----GTLPFSFSTSPSPGTAIFRPHEHMETHEVPSSIVV 247
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 175 RQLRECTRWADAEEIPIGRWITRSTPPGSDSTAPT-----QEPAEPQDLIASTVA 229
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 248 PKGMNSTENSSASVRPK-----VLSSIQETGTPDNTSSARKGEDVNKTPLNL 295
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 230 --GVVTVMGSSQPVVVTRGTNDNLIPVYCIIAAVVVGLVAYIAFKRNWSCQNKKQGANS 287
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 296 QVYNHQOQPHRHILKLLPSMEATGEK--SSTPLKGPKRGHPRONLKHFDINEHLPMW 353
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 288 RPVNQTPPPE-----GEKUHSOGSIIVSDS-----QSLH---DQQPH---- 320
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 354 IVLFLLLVVVIWVSIRKSRRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKVIYICNG 413
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db.	321	-----TQTASQALG-----	-----DGGYSSLPKARB-----	346
Qy	414	HGDIILKLVAAQVQSNKDIYQFLCNASEREVA	FNSNGYTDHHERAY-----AALQH	465
Db	347	-----VEKLLINGSAGDTWRHL-----	-----AGELGYQPEHIDSFTEACPV	389
Qy	466	WTIRGPEASLAQLISALRQHRNRNDVVEKI	494	
Db	390	WATO-DSATLDALLAALRRRIORADLVESL	417	

RESULT 13

T28623
hypothetical protein G2R - variola major virus
C/Species: variola major virus
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C/Accession: T28623
R/Massung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A/Title: Potential virulence determinants in terminal regions of variola smallpox virus
A/Reference number: Z20488; MUID:94088747; PMID:8264798
A/Accession: T28623
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-348 <NAS>
A/Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A/Experimental source: strain Bangladesh 1975
C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

	Query Match	6.08;	Score 206.5;	DB 2;	Length 348;
	Best Local Similarity	34.1%;	Pred. No. 2.6e-06;		
	Matches 44;	Conservative 12;	Mismatches 66;	Indels 7;	Gaps 2;
QY	65	LTCDKCPAGVYVEHCTNTSLRVCSSCPVGCTFTFRHENGIEBKCHDCSPCPWPMEIKLP	CA	124	
Db	41	LCLLSCPFGYASRLCDSKTNTQCTPCGSGTFTSRNNHLPAFLCSNGRCNSNQVETRSCN		100	
QY	125	ALTDRECTCPPGMF-----QSNATCAPHTVCPVGMGRKKGTETEDVRCKQCARGTFSD		178	
Db	101	TTHNRICECFGYLLKGSSGCKACVQSQTFCGIGYGV-SGHTSVGDVICSPCGFGHYSH		159	
QY	179	VPSVMVKCK	187		
Db	160	TVSSADKCE	168		

RESULT 14

D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, V.V.; Shchelkunov, S.N.; Sandakchchiev, L.S.
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakchchiev, L.S.

FEBS Lett. 319, 80-83, 1993
 A:Title: Genes of varicella and vaccinia viruses necessary to overcome the host protect
 A:Reference number: S32385; MUID:93202281; PMID:8384129
 A:Accession: S32385
 A:Molecule type: DNA
 A:Residues: 31-168 <SHC>
 A:Cross-references: EMBL:X69198
 A:Experimental source: strain India-1967, ssp. major
 C:Genetics:
 A:Gene: GAR
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F:32-66/Domain: NGF receptor repeat homology <NGF>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match	6.0%;	Score 206.5;	DB 2;	Length 349;
Best Local Similarity	34.1%;	Pred. No. 2.6e-06;		
Matches	44;	Conservative 12;	Mismatches 66;	Indels 7; Gaps 2
Qy	65	LTCDKCPAGYVYSEHCTNTSLRVCS	CPVCGFTFRHENGIEKHCDCSQCPWP	WMIEKLPCA 124
Db	42	LCCLSCP	PGGYASRLCDSKNTQCTCGSGYFTSRNNHLPACLS	CNGRCNSNQVETRSCN 101
Qy	125	ALTDRECTCP	PGMP-----QSNATCAPHTVCPV	GWGVRKKGTETEDYRCQCA
Db	102	TTNRI	CECSPGYVYLLKGSSGKACYSQTKCGI	GYV-SGHTSVGDVICSPCGFTYSH 160
Qy	179	VPSSVMCKK	187	
Db	161	TVSSADKCE	169	

RESULT 15
A42086
CD30 antigen precursor - human
N;Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C;Accession: A42086
R;Dukop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A;Title: Molecular cloning and expression of a new member of the nerve growth factor
A;Reference number: A42086;MUID:92154659; PMID:1310894

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Query Match      5.98; Score 205; DB 2; Length 595;
Best Local Similarity 20.2%; Pred. No. 6.6e-06;
Matches 131; Conservative 66; Mismatches 250; Indels 200; Gaps 24

Qy      30  LLLG--FLSTTTAQPQK--ASNLIGTYRH-VDRATGQVLTKDKCPAGTVVSEHCTWTS 84
      | | | | | : : : | : | : | : | : | : | : | : | : | : |
Db      5  LAALGLLFGALRAFPQDRPEDTCHGNPSHYDKAVRR--CCYRCPMGLEFPTQCCPQP 62

Qy      85  LRVSSCPVGTFTTHENGIEKCHDCSQCPWPMEIKLPCAALTDRECTPPGMF----- 138
      | : : : : | : : : | : : | : | : | : | : | : | : | : |
Db      63  TDCRKQCEPDYVLDADRCYTCACVTSRD---DLVEKTPCAWNSRRVCRCRGMFCSTSAV 119

```

```

QY 139 QSNATCAPHTVCPVGVNRKKGTETEDV-----RCKQCARGTF----- 176
Db 120 NSCARCFH5VCPAGMIVKFPGTAKNTVCEPASPGVSPACASPENCKEPPSSGTIPQAKP 179
QY 177 -----SDVPSSV----- 183
Db 180 TPVSPATSSASTMPVRGGTKLAQEAASKLFRAPDSPSSVGRPSRSDPGLSPTQPCPEGSD 239
QY 184 -----MKCKAYTDCILSONLVVVKPGTKETDNVCGTLPFSFSSSTSPSGTA- 228
Db 240 CRQCEPDYLDAGRCTACVCSRDDLVKFTPCANNSSRTCECRPGMICATSNASCAR 299
QY 229 IFPRPEHMETHEVPSTYVPKGMNSTESNASVVRPKVLSSIOEGTVPDNTSSARGKEDV 288
Db 300 CVFYP-----ICAAETVTKPQDMAEKDTFEAPPL-----GTQPCDCNPTPENGAP 345
QY 289 NKTLPNLQVNVHOGPHRHILKLLPSMEATGGEKSTPIKPKRGHPRONLHKHEDINE 348
Db 346 ASTSPTQSLVDSQAS-----KTLPI-----PTSAPVALSSTGKP-----VLDAGP 386
QY 349 HLPWMIVFLLLVLVIV-----VGSIRKSSRTLKKG-----PRODPSAIVEKAGLKS 397
Db 387 VLEWVI-----LVVVVVGSSAFLLCHRRACRRIRQKHLHCYPVQTSQPKLELVDSRPR 441
QY 398 MPTQNRKWIYYCNGHGDILKLVAQVGSQWKDIYQFLCNASEREVAFAFSNGYTADHE 457
Db 442 RSTQLRS-----GASVTEPVAEERGLMSQPLME-TC-----HS 474
QY 458 RAYAAALQHWITR-----GPEASLAQLISALRQHRNDVVEKIRGLMEDTTOLETKLAL 511
Db 475 VGAAYLESPLQDASPAGGSPRDLPEPRVSTEHTNNKIEKIYIMKADTVIVGTVAEL 534
QY 512 PMSPSPLSPSPIPSPNAKLENSALLAVEPSPQDNKGFFVDESEPLL 558
Db 535 PEGRGLAGPAE-PELEEELE-----ADHTPHYPEQETEPEPL 569

```

Search completed: July 11, 2003, 15:49:32
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:47:23 ; Search time 25 Seconds
(without alignments)
1086.680 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

Sequence: 1 MGTSPSSSTALASCRIARR.....SQEASQTLDSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3456	100.0	655	1 TR21_HUMAN	O75509 homo sapien
2	3059	88.5	655	1 TR21_MOUSE	Q9epu5 mus musculus
3	343.5	9.9	461	1 TR1B_HUMAN	P20333 homo sapien
4	304.5	8.8	401	1 T11B_RAT	O08727 rattus norv
5	301.5	8.7	401	1 T11B_HUMAN	O00300 homo sapien
6	301.5	8.7	401	1 T11B_MOUSE	O08712 mus musculus
7	287	8.3	300	1 TR6B_HUMAN	O95407 homo sapien
8	273.5	7.9	474	1 TR1B_MOUSE	P25119 mus musculus
9	238	6.9	415	1 TR3_MOUSE	P50284 mus musculus
10	236.5	6.8	416	1 TR16_CHICK	P18519 gallus gall
11	235.5	6.8	255	1 TR9_HUMAN	O07011 homo sapien
12	233	6.7	289	1 TR5_MOUSE	P27512 mus musculus
13	228.5	6.6	435	1 TR3_HUMAN	P36941 homo sapien
14	227	6.6	269	1 TR5_BOVIN	Q28203 bos taurus
15	218.5	6.3	326	1 V72_MYXVL	P29825 myxoma viru
16	215.5	6.2	351	1 CRMB_COMPX	O73559 cowpox viru
17	211.5	6.1	325	1 V72_SFVKA	P25943 shope fibro
18	211.5	6.1	425	1 TR16_RAT	P07174 rattus norv
19	210.5	6.1	427	1 TR16_HUMAN	P08138 homo sapien
20	208.5	6.0	349	1 CRMB_CAMPS	Q8uay7 camelopox vi
21	206.5	6.0	349	1 CRMB_VARV	P34015 variola vir
22	206	6.0	625	1 TR11_MOUSE	O35305 mus musculus
23	205.5	5.9	616	1 TR11_HUMAN	Q9y6q6 homo sapien
24	205	5.9	283	1 TR14_HUMAN	O92956 homo sapien
25	205	5.9	595	1 TR8_HUMAN	P28908 homo sapien
26	200	5.8	277	1 TR5_HUMAN	P25942 homo sapien
27	199.5	5.8	417	1 TR16_MOUSE	Q920w1 mus musculus
28	195	5.6	471	1 TR16_BOVIN	O19131 bos taurus
29	193	5.6	461	1 TR1A_PIG	P50555 sus scrofa
30	187.5	5.4	493	1 TR8_RAT	P97525 rattus norv
31	186.5	5.4	461	1 TR1A_RAT	P22934 rattus norv
32	180.5	5.2	256	1 TR9_MOUSE	P20334 mus musculus
33	176	5.1	498	1 TR8_MOUSE	Q60846 mus musculus

RESULT 1

ID	TR21_HUMAN	STANDARD:	PRT:	655 AA.
AC	O75509; Q96D86;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-DE related death receptor-6) (Death receptor 6).			
GN	TNFRSF21 OR DR6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98378343; PubMed=9714541;			
RA	Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;			
RT	"Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";			
RL	FEBS Lett. 431:351-356(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Parker A.;			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Colon;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.			
CC	-!- SUBUNIT: Associates with TRADD.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).			
CC	-!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.			
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF068868; AAC34583.1; -			
DR	EMBL; AL096801; CAB75692.1; -			
DR	EMBL; BC017730; AAH17730.1; -			
DR	EMBL; BC10241; AAH10241.1; AUT_INIT.			
DR	Genew; HGNC:13469; TNFRSF21.			

34	175	5.1	176	1	TR23_MOUSE	Q9er63 mus musculus
35	170	4.9	454	1	TR1A_MOUSE	P25118 mus musculus
36	162	4.7	259	1	T10C_HUMAN	O14798 h tumor nec
37	154	4.5	277	1	TNR4_HUMAN	P43489 homo sapien
38	149.5	4.3	1193	1	LMG2_HUMAN	Q13753 homo sapien
39	148	4.3	271	1	TNR4_RAT	P15725 rattus norv
40	146	4.2	180	1	TR22_MOUSE	Q9er62 mus musculus
41	145.5	4.2	455	1	TR1A_HUMAN	P19438 homo sapien
42	142	4.1	417	1	TR12_HUMAN	Q93038 h tumor nec
43	136	3.9	272	1	TNR4_MOUSE	P47741 mus musculus
44	135.5	3.9	5376	1	ZAN_MOUSE	O88799 mus musculus
45	131.5	3.8	440	1	T10B_HUMAN	O14763 homo sapien

ALIGNMENTS

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DR MTM; 605732; -.
DR HSP; O14763; 1D0G.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 100.0%; Score 3456; DB 1; Length 655;
Best Local Similarity 100.0%; Pred. No. 9,8e-220;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSALASCRIARRATMIAGSLLLGLSTTTAAQPEQKASNLIGTYRHVDRA 60
DB 1 MGTSPSSALASCRIARRATMIAGSLLLGLSTTTAAQPEQKASNLIGTYRHVDRA 60

QY 61 TGOVLTCDCPCAGTYVYVSEHCTNTSLRVCSCPVGTFTRHENGIEKCHDCSQPCWPWIEK 120
DB 61 TGOVLTCDCPCAGTYVYVSEHCTNTSLRVCSCPVGTFTRHENGIEKCHDCSQPCWPWIEK 120

QY 121 LPCAALTDRECTCPGCFMFSNATCAPHTVCPVGWGVKKGTEDETRVRCQKARGTSDVP 180
DB 121 LPCAALTDRECTCPGCFMFSNATCAPHTVCPVGWGVKKGTEDETRVRCQKARGTSDVP 180

QY 181 SSVMKCKAYTDCLSQNLVVKPCTKETDNVCGTLPFSFSSSTSPSCPTAIFPRPEHMETHE 240
DB 181 SSVMKCKAYTDCLSQNLVVKPCTKETDNVCGTLPFSFSSSTSPSCPTAIFPRPEHMETHE 240

QY 241 VPSSTVYVPGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVAKTLPNLQVNH 300
DB 241 VPSSTVYVPGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVAKTLPNLQVNH 300

QY 301 QQGPHRHLKLLPSEATGGEKSTPIKGRKGRHPQNLHKHFDNEHLPMWIVFLLL 360
DB 301 QQGPHRHLKLLPSEATGGEKSTPIKGRKGRHPQNLHKHFDNEHLPMWIVFLLL 360

QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYVNCNGHGDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYVNCNGHGDILK 420
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QY 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAQLQHWITIRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAQLQHWITIRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETGDKLALPNSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETGDKLALPNSPSPSPSPSPSPSPSPSPSPSPSPSPSP 540

QY 541 SPQDNKNGFFVDESEPLLCDSSTSSGSSALSRRNGSFTITREKDKDTVLQVRLDPCDLQPIF 600
DB 541 SPQDNKNGFFVDESEPLLCDSSTSSGSSALSRRNGSFTITREKDKDTVLQVRLDPCDLQPIF 600

QY 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLLDSVYSHLPDLL 655
DB 601 DDMHLFNLPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLLDSVYSHLPDLL 655

RESULT 2
TR21_MOUSE STANDARD; PRT; 655 AA.
AC Q9EPUS: Q9LXH9; Q9LW77;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-x., Wang X., Cal Z.;
RT "Murine DR6: murine TNFR-related death receptor-6.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION
RX MEDLINE=21571606; PubMed=11714751;
RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell
RT differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448(2001).
CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC similarity). May activate JNK and be involved in T-cell
CC differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC thymus, testis, prostate, ovary, small intestine, colon, brain,
CC lung and kidney, and in fetal brain, liver and lung. Detected at
CC lower levels in adult peripheral blood leukocytes, lung, and in
CC fetal muscle, heart, kidney, small intestine and skin. Detected in
CC T-cells, B-cells and monocytes. In T-cells expression is highest
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
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CC DR EMBL; AF322069; AAG38115.1; -
CC DR EMBL; AY043489; AAK74193.1; -
CC DR EMBL; BC016420; AAHL6420.1; -
CC DR HSSP; O14763; IDOG.
CC DR MGD; MGI:2151075; Tnfrsf21.
CC DR InterPro; IPR000488; Death.
CC DR InterPro; IPR001368; TNFR_c6.
CC DR Pfam; PF00020; TNFR_c6; 4.
CC DR ProDom; PD000771; TNFR_c6; 1.
CC DR SMART; SM00005; DEATH; 1.
CC DR SMART; SM00208; TNFR; 4.
CC DR PROSITE; PS0017; DEATH_DOMAIN; 1.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 1.
CC DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT FT
FT FT
FT DOMAIN 42 349
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT REPEAT 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
FT CARBOHYD 82 82
FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 289
FT CARBOHYD 289 289
FT CONFLICT 352 352
FT CONFLICT 523 523
SQ SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99EFF7 CRC64;

Query Match 88.5%; Score 3059; DB 1; Length 655;
Best Local Similarity 88.9%; Pred. No. 1.2e-193;
Matches 583; Conservative 19; Mismatches 52; Indels 2; Gaps 2;

QY 1 MGTSPSSALASCRIARRATATMIAGSLLLGLFTTTTAQPEKQKSNLIGTVRHVDRA 60
DB 1 MGTASSITALLSCLSSRTAGQGVATWAGSLLLGLFTSTTAQPEKTLSPGTVRHVDRT 60

QY 61 TGOVLTCDCPAGTVVSEHCNTSLRVCSGPCVGTFTRHENGIEKHCDCPCPCWPMIEK 120
DB 61 TGOVLTCDCPAGTVVSEHCNTNMSLRVCSGPCAGTFTRHENGIERCHDCSCPCWPMIEK 120

QY 121 LPCAALTDRECTCPGMPQSNATCAPHTVCVPVGVGVRKKGTETEDVRCCKQCARGTFSVDP 180
DB 121 LPCAALTDRECTCPGMPQSNATCAPHTVCVPVGVGVRKKGTENEDVRCCKQCARGTFSVDP 180

QY 181 SSVMKCKAYTDCQLQNLVWIRKPTKETDNVCGTLPSPSSSTSPSPGTAIFPRPEHMETHE 240
DB 181 SSVMKCKAHTDCQLQNLVWIRKPTKETDNVCGMLFFSSTNPPSPSGTFTFSHPHEHMSHD 240
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QY 241 VPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNTKLPNLQVNH 300
DB 241 VPSSTYEPQGMNSTDSNSTASVRKVPFGIEEGTVPDNTSSTSGKECTNRTLPNPQVTH 300

QY 301 QQGPHHRIKLKLP-SMEATGGEKSSPTPIGPKRGHPRQNHKHFIDINEHLPWMIVLFL 359
DB 301 QQAPHHRIKLKLPSSMEAT-GEKSSTAIRKAPRGHPRQNAHKHFIDINEHLPWMIVLFL 359

QY 360 LVLVIVVVCSTRKSSRTLKKGPDPDPSAIVEKAGLKSKMTPQNRKWIYCNCGHGIDIL 419
DB 360 LVLVIVVCSIRKSSRTLKKGPDPDPSAIVEKAGLKSKSLTPQNRKWIYRNCGHGIDIL 419

QY 420 KLVAQVGSQWKDIYQFLCNASEREVAAFNGYTDHERAYAAALQHWITIRGPEASLAQLI 479
DB 420 KLVAQVGSQWKDIYQFLCNASEREVAAFNGYTDHERAYAAALQHWITIRGPEASLAQLI 479

QY 480 SALRQHRNDVVEKIRGLMEDTTQETDKKALPMSPSPSPSPSPSPSPSPSPSPSPSPSP 539
DB 480 SALRQHRNDVVEKIRGLMEDTTQETDKKALPMSPSPSPSPSPSPSPSPSPSPSPSPSP 539

QY 540 PSpODKNGGFVDESEPLLRCDSTSGSSALSRLNGSFITKEKDTVLQVRLDPCDQPI 599
DB 540 PSpLDKNGKCFVDESEPLLRCDSTSGSSALSRLNGSFITKEKDTVLQVRLDPCDQPI 599

QY 600 FDDMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSVYSHLPDLL 655
DB 600 FDDMLHIINPEELRVIEEIPQAEKDLRLFEIIGVKQSEASQTLSDSVYSHLPDLL 655

RESULT 3
TRIB_HUMAN STANDARD; PRT; 461 AA.
ID AC P20333; O16042;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (p80) (TNFR-R2) (p75) (CD120b) (Etanercept)
DE [Contains: Tumor necrosis factor binding protein 2 (TNFR2)].
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RA "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins."
RT Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene."
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
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Oy . 234 ----EHMETHEVPS-----STYVPGKMNSTESNS----- 259
Db 221 STRSQHTQPTPEPSTAPSTSTFLLPMGPSPPAEGSTGDFALPVGLVGTALGLLLIGVWN 280
Oy 260 ----ASVRPKVLSSIQEGTVPD-NYSSARGKEDVKNKTLPNLVQVNHQOGPHRRHILKLP 314
Db 281 CVIMTQVKKKPLCLQREAKVPHLPADKARG-----TOGPEQOHLITAP 324
Oy 315 SMEATGGEKSTPT--KGPKRGHPR 337
Db 325 SSSSSLESSASALDRAPTRNQPO 349

RESULT 4
TILB_RAT
ID TILB_RAT STANDARD; PRT; 401 AA.
AC O08727;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).

-1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC
CC -1- SUBUNIT: Homodimer (By similarity).
CC
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC
CC -1- INDUCTION: Upregulated by osteopontin.
CC
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
CC -1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC
CC
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CC
CC -----
DR EMBL; U94330; AAB53707.1; -.
DR HSSP; P25942; 1CDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.

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FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 11B.
FT REPEAT 24 62 TNFR-CYS 1.
FT REPEAT 65 105 TNFR-CYS 2.
FT REPEAT 107 142 TNFR-CYS 3.
FT REPEAT 145 185 TNFR-CYS 4.
FT DOMAIN 198 269 DEATH 1.
FT DOMAIN 270 365 DEATH 2.
FT SITE 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT DISULFID 166 185 BY SIMILARITY.
FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 401 AA; 46192 MW; FEC6A31FID4E573A CRC64;

Query Match 8.8%; Score 304.5; DB 1; Length 401;
Best Local Similarity 28.6%; Pred. No. 5.8e-13;
Matches 91; Conservative 44; Mismatches 142; Indels 41; Gaps 9;

Oy 30 LLLGLFLSTTAQ--PEQKASNLIGTYRHVDRTAGQVLTCDKCPAGTYVSHCHTNTSLRV 87
Db 10 LVFLDIIEWTTFETFPK-----YLHYDPTGTQLLCKDKCAPGYLKHQCHVRRKLT 61
Oy 88 CSSCPVCTFFRHENGIEKHCDCSQPCWPMEIKLPALCAALTDRECTCPGWFQSNATCAPH 147
Db 62 CVPCPDYSYDSDSWHTSDCEVYCSVCKELQTVQKCEKTRHNRVCECEGRYLEFCLKH 121
Oy 148 TVCPGVGVRKKGKGTETEDVRCKQCARGTFSDVPSVMKCKAYTDCLSQNLVYIKPGTKET 207
Db 122 RSCPPGLGVLAGTGPRTNTVCKRCPDGFSGSETSKAPCRKHTNCSSLLGLLLQKGNATH 181
Oy 208 DNVCGTLPSSSTSPSPGTAIFRPRHEMETHVPSTTYVPKGMN-----STESNSA 260
Db 182 DNVG-----SGNREATCGIDVTLCCEAFFRFAVPTK-IIPNWLVLVDSLPGTKVNAES 236
Oy 261 SVRPKVLSSIQEGTVP-----DNTSSARGKEDVKNKTLPNLVQVNHQOGPHRRHI---- 309
Db 237 VERIKRRHSSQEQTFQLLKLWKHON-----RDQEMVKLIQDIDLCSSVQRHIGHANLTT 292
Oy 310 --LKLPSMEATGGEKSS 325
Db 293 EQLRIL--MESLPGKKIS 308

RESULT 5
TILB_HUMAN
ID TILB_HUMAN STANDARD; PRT; 401 AA.
AC O00300; O60236; Q9UHP4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,

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RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombo A., Tan H.-L., Trill G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RT Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro";
RT Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RX Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor";
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN [6]
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens";
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN [7]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis";
RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN [8]
RP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Dean K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dods R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL";
RL J. Biol. Chem. 273:14363-14367(1998).
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor";
RL J. Biol. Chem. 273:5117-5123(1998).
RN [10]
RP REVIEW.
RX MEDLINE=21395914; PubMed=11505389;

RA Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases";
RL Cancer 92:460-470(2001).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and skeletal
CC muscle. Highly expressed in fetal kidney, liver and lung.
CC -!- INDUCTION: Upregulated by increasing calcium-concentration in the
CC medium and estrogens. Downregulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains sialic acid residues.
CC -!- PTM: N-terminus may be blocked.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC -----
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CC -----
DR EMBL; U94332; AAB53709.1; -;
DR EMBL; AB002146; BAA25910.1; -;
DR EMBL; AB008822; BAA32076.1; -;
DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; BC030155; AAB30155.1; -;
DR EMBL; AF134187; AAF20168.1; -;
DR HSSP; P25942; ICDP.
DR Genew; HGNC:11909; TNFRSF11B.
DR MIM; 602643; -;
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 401
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 11B.
FT REPEAT 24 62
FT TNFR-CYS 1.
FT REPEAT 65 105
FT TNFR-CYS 2.
FT REPEAT 107 142
FT TNFR-CYS 3.
FT REPEAT 145 185
FT TNFR-CYS 4.
FT DOMAIN 198 269
FT DEATH 1.
FT DOMAIN 270 365
FT DEATH 2.
FT SITE 400 400
FT INVOLVED IN DIMERIZATION.
FT DISULFID 41 54
FT BY SIMILARITY.
FT DISULFID 44 62
FT BY SIMILARITY.
FT DISULFID 65 80
FT BY SIMILARITY.
FT DISULFID 83 97
FT BY SIMILARITY.
FT DISULFID 87 105
FT BY SIMILARITY.
FT DISULFID 107 118
FT BY SIMILARITY.
FT DISULFID 124 142
FT BY SIMILARITY.
FT DISULFID 145 160
FT BY SIMILARITY.
FT DISULFID 166 185
FT BY SIMILARITY.
FT CARBOHYD 98
FT N-LINKED (GLCNAC...) (POTENTIAL).

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FT CARBOHYD 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 3 K -> N.
FT /FTid=VAR_013439.
FT MUTAGEN 400 C->S: ABOLISHES DIMERIZATION.
FT MUTAGEN 400 MISSING: ABOLISHES DIMERIZATION.
FT CONFLICT 263 D -> A (IN REF. 1).
SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;

Query Match 8.7%; Score 301.5; DB 1; Length 401;
Best Local Similarity 24.8%; Pred. No. 9.1e-13;
Matches 102; Conservative 58; Mismatches 177; Indels 75; Gaps 13;

QY 54 YRHVDRTGVLTKCDKCPAGYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPC 113
DB 28 YLHDETSHQLLCKDPPGYLQKHCTAKWKTVCAPCPDHYHDTSDWHTSDECIYCSQVC 87
QY 114 PPMIEKLPCALTDRECTCPGFMFSQSNATCAPHTVCPVGMGVRKKGTTETEDVRCKQCAR 173
DB 88 KELQVQECNRTHNRVCECKEGRYLETEFCLKHRSCPPGGVGVQAGTPERTNVTCKRCPD 147
QY 174 GTFSDVPSSVMKCAKAYTCLSONLVKPKGTEDNVCGLTLPFSSTSPSPGTAIPRP 233
DB 148 GFFSNETSSKAPCRKHTNCVSFGLLTQKGNATHDNC-----SGNSESTQKCGIDVTLC 203
QY 234 EHMETHEVPSSTYVPKGMN-----STESNSSASVRPKVLSSTQEGTVP-----DNT 279
DB 204 EAFTRFAVPTK-FPNWLSVLVDNLPGTKVNAESVERIKRQHSQEQTFQLLKWKHQN- 261
QY 280 SSARGKEDVNTLPNLQVNHQOQPHRH-----ILKLLPSMEATGKESSTPIK 329
DB 262 ---KQDQIVKIIQIDILCENSQVRHIGHANLTPEQLRSLMESLPG-KKVGAEDIEKTIK 317
QY 330 GPKRGHPRONLKHFFDINEHLPWMLVLELLVLVIVVCSIRKSRLLKKGPRQDPSAIV 389
DB 318 ACK---PSDQTLKLLSL---WRI-----KNGDQDTLKLGLM 346
QY 390 EKAGLKKS-----MTPTQNKWIIYVNGHGIDIL--KLVAAGVGSQWKDI 433
DB 347 H--ALKHSKTHFFKTVTQSLKKTIRFLHSTMYTKLKQLKPLEMIGNQVQSV 396

RESULT 6
T11B_MOUSE
ID T11B_MOUSE STANDARD; PRT; 401 AA.
AC 008712; 070202;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPB OR OCIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
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RP AND ARG-296.
RX STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
RN [3]
RP FUNCTION.
RX MEDLINE=21060987; PubMed=10952716;
RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT osteoclasts and prevents vascular calcification by blocking a process
RT resembling osteoclastogenesis.";
RL J. Exp. Med. 192:463-474(2000).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC intestines and calvaria. Highly expressed in decidua and placenta,
CC and in embryo.
CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
CC whereas expression decreases at day 11 and increases from day 15
CC to 17. On day 15' found in developing bone primordia,
CC brachiocephalic artery and ductus arteriosus, left main bronchus,
CC abdominal aorta and midgut.
CC -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC -----
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CC -----
DR EMBL; U94331; AAB53708.1; -.
DR EMBL; AB013898; BAA28269.1; -.
DR EMBL; AB013903; BAA33388.1; -.
DR EMBL; AB013899; BAA33388.1; JOINED.
DR EMBL; AB013900; BAA33388.1; JOINED.
DR EMBL; AB013901; BAA33388.1; JOINED.
DR EMBL; AB013902; BAA33388.1; JOINED.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:109587; Tnfrsf11b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS06552; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
FT REPEAT 24 62 TNFR-CYS 1.
FT REPEAT 65 105 TNFR-CYS 2.
FT REPEAT 107 142 TNFR-CYS 3.
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FT REPEAT 145 185 TNFR-CYS 4.
FT DOMAIN 198 269 DEATH 1.
FT SITE 283 365 INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT DISULFID 166 185 BY SIMILARITY.
FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH
FT VARIANT 161 161 SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
FT VARIANT 165 165 SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
FT VARIANT 296 296 SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 8.7%; Score 301.5; DB 1; Length 401;
Best Local Similarity 29.0%; Pred. No. 9.1e-13;
Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;

QY 30 LLLGLSLSTTAPEQKASNLIGTYRHVDRAVGTLTCDKCPAGTVVSEHCTNLSRVCS 89
DB 10 LVLLDIETWTE-----TLPPKYLHYDEPTGHQLLDCAPGTVLKQHCIVRRKTLCV 63
QY 90 SCVPGFTTHRENGIEKCHDCSPQCPWPMIEKLPCAALTIRECTCPGPMFSNATCAPHTV 149
DB 64 PCPDHSYTDSWHTSDCEVCVCKELQSVKQECNTRNVCBCEGRYLETEFCLKHRS 123
QY 150 CPVGWVRKKGTEDEVCKCARGTFSDVPSSVMCKKAYTDCLSQNLVVRPGTKETDN 209
DB 124 CPPGSGVAGVGPRTNVCVKCPDGFSGTSCAPCIKHCNCTFGLLLIQGNATHDN 183
QY 210 VCTLPSFSSSTSPSPGTAIFRPEHMETHEVPSSTYVPKGMN-----STESNSSASV 262
DB 184 VC-----SGNREATQKCGIDVTLCEEAFFRFAVPTK-IIPNLSVLVDLSLPGTKVNAESVE 238
QY 263 RPKVLSIOEGTVP-----DNTSSARGKEDVKNLPLQVNVHQQGPHHRH-----ILK 311
DB 239 RIKRRHSSQEQTFQLLKLKHQN---RDQEMVKKIQIDLCSSVQRHLGHSNLTTEQ 294
QY 312 LLPSMEATGKSS 325
DB 295 LLALMESLPKKIS 308

RESULT 7
TR6B_HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC Q95407;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
GN receptor for Fas ligand) (Decoy receptor 3) (Dcr3) (M68).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
CC and TNFSF6/FasL. Protects against apoptosis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
CC Detected in adult stomach, spinal cord, lymph node, trachea, tumors
CC spleen, colon and lung. Highly expressed in several primary tumors
CC from colon, stomach, rectum, esophagus and in SW480 colon
CC carcinoma cells.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
CC EMBL: AF104419; AAD03056.1; -
CC EMBL: AF134240; AAD29688.1; -
CC EMBL: AF217796; AAF35244.1; -
CC EMBL: AF217793; AAF33685.1; -
CC EMBL: AF217794; AAF33686.1; -
CC EMBL: AL121845; CAC03668.1; -
CC EMBL: BC017065; AAH17065.1; -
CC Genew; HGNC:11921; TNFRSF6B.
CC MIM; 603361; -
CC HSP; O14763; ID0G.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 4.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS0050; TNFR_NGFR_2; 2.
CC Receptor; apoptosis; Glycoprotein; Repeat; Signal.
CC SIGNAL 1 29
FT
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FT CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR
FT REPEAT 31 70 SUPERFAMILY MEMBER 6B.
FT REPEAT 72 113 TNFR-CYS 1.
FT REPEAT 115 150 TNFR-CYS 2.
FT REPEAT 152 193 TNFR-CYS 3.
FT REPEAT 152 193 TNFR-CYS 4.
FT DISULFID 49 62 BY SIMILARITY.
FT DISULFID 52 70 BY SIMILARITY.
FT DISULFID 73 88 BY SIMILARITY.
FT DISULFID 91 105 BY SIMILARITY.
FT DISULFID 95 113 BY SIMILARITY.
FT DISULFID 115 126 BY SIMILARITY.
FT DISULFID 132 150 BY SIMILARITY.
FT DISULFID 153 168 BY SIMILARITY.
FT DISULFID 174 193 BY SIMILARITY.
FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 300 AA; 32679 MW; F90AE3371849AF CRC64;

Query Match 8.3%; Score 287; DB 1; Length 300;
Best Local Similarity 34.3%; Pred. No. 5.7e-12;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;

QY 53 TYRHVDRATGQVLCDCPCAGTYVSEHCTNLSRVCSGPCVGTTRHNGIEKCHDCSQP 112
DB 35 TYPRDAETGERLYCAQCPGTFYQPCRRDSPTTCGPPRPHYTFWNYLERCRYCNVL 94

QY 113 CPWPMEIKLPAAALTDRECTCPGCMFQSNATCAPHTVCPGCMGVKKGKTETEDVRCKOCA 172
DB 95 CGEEREERACHATHNRACRGTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQOCPCP 154

QY 173 RGTESDVPSSVMKCAKAYTDCILSONLVIKPKTKETDNVCGTLPFSFST 221
DB 155 PGTFSSSSSEQCPHNRNCALGALNVPSSSHDTLCTCTGFPPLST 203

RESULT 8
TRIB_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026 (1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.

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RC TISSUE=Liver;
RA Kissinger M., Fellows R., Feldmann M., Chernajovsky Y.;
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSF1/lymphotoxin-alpha (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; M60469; AAA39752.1; -
DR EMBL; M59378; AAA40463.1; -
DR EMBL; U39488; AAA85021.1; -
DR EMBL; X87128; CAA60618.1; -
DR PIR; B38634; B38634.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrrsflb.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 23 258 SUPERFAMILY MEMBER 1B.
FT TRANSMEM 259 288 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 7.9%; Score 273.5; DB 1; Length 474;
Best Local Similarity 25.0%; Pred. No. 7.8e-11;
Matches 82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;

QY 65 LTCDKCPAGTYVSEHCTNLSRVCSGPCVGTTRHNGIEKCHDCSQPCPWPMEIKLPCA 124
DB 53 MCCAKCPGPGVYKHFCNKTSDTVCADCEASMYTQVWNOFRTCLSCSCTTDDQVEIRACT 112

QY 125 ALTDRETCPPGMFQSNAT-----CAPHTVCPGCMGVKKGKTETEDVRCKOCARGTFS 177
DB 113 KOQNRVCAEAGRYCALKTHSGSCRCQCMRLSKCGFGVASSRAPNGNVLKACAPGTF 172

QY 178 DVPSSVMKCAKAYTDCILSONLVIKPKTKETDNVCGTLPFSFSSSTSPSPGTAIFPRPEHME 237
DB 173 DTTSTSDVCRPHRIC-----SILAIPGNASTAVCA-----PESPT 208

QY 238 THEVPSSTYV-----PKGMMNSTESNASSVRPKVLSSIQEGTVPDNTSSARGKDVNKTLP 293

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Db 209 LSAIPRTLYVSQPEPTRSRPLDQEPGSPQTSILTSL--GSTPIIEQSTKG-----GISLP 262
QY 294 -----NLQWVN-----HQQGP-----HRHLK 311
Db 263 IGLIVGVTSLGLMLGLVNCILIVQRKKPKCLORDAKVHPVDPDEKSDQAVGLEQQHLIT 322
QY 312 LPLSMEATGGEKSSST--PIKPKRGHPR 337
Db 323 TAPSSSSSSLESSASAGDRRAPPGGHPQ 350
RESULT 9
TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor).
GN LTBR OR TNFRSF3 OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RT Browning J.D., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT The murine lymphotoxin-beta receptor cDNA: Isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs
CC (By similarity).
CC -!- SUBUNIT: Self-associates (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U29173; AAA68964.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAA81334.1; -
DR HSSP; O14763; ID0G.
DR MGD; MGI:104875; Ltbr.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 3.

FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;
Query Match 6.9%; Score 238; DB 1; Length 415;
Best Local Similarity 23.5%; Pred. No. 1.4e-08;
Matches 95; Conservative 40; Mismatches 144; Indels 126; Gaps 17;
QY 16 RIARRATATMIAGSLLLGLFLSTTTTAQPEQKASNLIGTYRHVDRA-----GQV 64
Db 2 RLPRASSPCGLAWGPLLLGLGLVASQPQ---LVPPYR-IEQTCWDQDKEYEYPMHD 56
QY 65 LTCDKCPAGTYVEHCTNTSLRVCSCPVGTFTTRHENGIEKHCDCSQCPWPM--LEKLP 122
Db 57 VCCSRCPGGEFVAVGSRSDQTVCKTCTPHNSYNEHWNHLSLTCQLC-RPCDIVLGFEVAP 115
QY 123 CAALTDRECTCPGPM---EQSN-----ATCAPHTVCPVGVGVRKKGTE----- 164
Db 116 CTSDRKAECRCQGMSCVYLDNECVHCEERLVLCOP-----GTAEVYDEI 162
QY 165 ---DVRCKQARGTFSDVPSSVMKAYTDCLSQNLVVIKPGTKTDNVCGTLPS----- 216
Db 163 MDTDVNCVCKPGHFQNTSSPRARCQPHTRCEIQGLVEAAAGTSTYDICKNPPEGAML 222
QY 217 -----FSS-----STSPSGCTAIFPRPEHMETHEVSPSTVVPKGMNS 253
Db 223 LLAILLSLVFLFTTTLACAMMRHPSLCRKLGLTLKRHPGEGEESPPCAPRADPH----- 278
QY 254 TESNSASVRPKVLSIIQGTVP---DNTSSARGKEDVANKTLPNL-OVYNHQQGP----- 304
Db 279 -----FPDLAEPLPMSGDLSPSPAGP---PTAPSLVEVVLQQSPLVQAR 321
QY 305 -----HHRHLKLLPSMEATGGEKSS-----PIKPKRG 334
Db 322 ELEAEPGEHQVAHGANGIHVTGGSVTVGTGNIYNGPVLGGTRG 366
RESULT 10
TNR16_CHICK STANDARD; PRT; 416 AA.
AC P18519;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;


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DR  EMBL; M94128; AAA37404.1; JOINED.
DR  EMBL; M94127; AAA37404.1; JOINED.
DR  EMBL; AJ401387; CAC29427.1; -.
DR  EMBL; AJ401388; CAC29428.1; -.
DR  EMBL; AJ401389; CAC29429.1; -.
DR  EMBL; AJ401390; CAC29430.1; -.
DR  PIR; A46476; A46476.
DR  HSP; P25942; ICDF.
DR  MGD; MGI:88336; Tnfrsf5.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00020; TNFR_c6; 4.
DR  ProDom; PD000771; TNFR_c6; 1.
DR  SMART; SM00208; TNFR; 4.
DR  PROSITE; PS00652; TNFR_NGFR_1; 1.
DR  PROSITE; PS00652; TNFR_NGFR_2; 4.
KW  Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW  Alternative splicing.
FT  SIGNAL 1 19
FT  CHAIN 20 289
FT  DOMAIN 20 193
FT  TRANSMEM 194 215
FT  DOMAIN 216 289
FT  REPEAT 25 60
FT  REPEAT 61 103
FT  REPEAT 104 144
FT  REPEAT 145 187
FT  DISULFID 26 37
FT  DISULFID 38 51
FT  DISULFID 41 59
FT  DISULFID 62 77
FT  DISULFID 83 103
FT  DISULFID 105 119
FT  DISULFID 111 116
FT  DISULFID 125 143
FT  CARBOHYD 153 153
FT  VARSPLIC 166 203
FT  VARSPLIC 204 289
FT  VARSPLIC 187 216
FT  VARSPLIC 216 234
FT  VARSPLIC 235 289
FT  VARSPLIC 216 222
FT  VARSPLIC 223 289
SQ  SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA57AE CRC64;
Query Match 6.7%; Score 233; DB 1; Length 289;
Best Local Similarity 34.9%; Pred. No. 1.9e-08;
Matches 53; Conservative 21; Mismatches 70; Indels 8; Gaps 4;
QY 67 CDKPCAGYVSEHCNTSLRVCSSCPVTFTRHENGIEKCHD---CSOPCPWPMEIKLPC 123
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38 CDLCOPGSLRTSLALEKTQCHPCDSCGEFSAQNNREIRCHQHRHC-EPNQLRVKK-EG 95
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 124 AALTDRECTCPGPMFSQN---ATCAPHTVCPVGVKKGTEDETVRCCKQCAARGTFSDVP 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 96 TAESDTVCTCKEGQCHTCKDECAQAQHTPCIPGFGVMEYATETDVTCHPCPVGFFSNQS 155
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 SSVMKCKAYTDCLSQNLVVIKPGTKETDNVCG 212
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 156 SLFEKCYDPTSCEDKNLEVLQKGTSTQTNVICG 187
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 13
ID TNR3_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
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DE DE EMBL; M94128; AAA37404.1; JOINED.
DE DE EMBL; M94127; AAA37404.1; JOINED.
DE DE EMBL; AJ401387; CAC29427.1; -.
CN GN EMBL; AJ401388; CAC29428.1; -.
OS EMBL; AJ401389; CAC29429.1; -.
OC EMBL; AJ401390; CAC29430.1; -.
OX PIR; A46476; A46476.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RL transcribed sequences derived from a somatic cell hybrid.";
RN Genomics 16:214-218(1993).
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RT Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RL "A lymphotoxin-beta-specific receptor.";
RN Science 264:707-710(1994).
RP CHARACTERIZATION.
RX MEDLINE=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RN death in HeLa cells";
RN J. Biol. Chem. 274:11868-11873(1999).
RP FUNCTION.
RX MEDLINE=10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RT Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RN LIGHT-mediated apoptosis of tumor cells.";
RN J. Biol. Chem. 275:14307-14315(2000).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB5, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -!- SUBUNIT: Self-associates.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; L04270; AAA36757.1; -.
DR EMBL; BC026262; AAH26262.1; -.
DR HSP; P25942; ICDF.
DR Genew; HGNC:6718; LTBR.
DR MIM; 600979; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 3.

FT	DOMAIN	31	227	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	228	248	POTENTIAL.
FT	DOMAIN	249	435	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	42	81	TNFR-CYS 1.
FT	REPEAT	82	124	TNFR-CYS 2.
FT	REPEAT	125	168	TNFR-CYS 3.
FT	REPEAT	169	211	TNFR-CYS 4.
FT	DISULFID	43	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	80	BY SIMILARITY.
FT	DISULFID	83	98	BY SIMILARITY.
FT	DISULFID	101	116	BY SIMILARITY.
FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	148	BY SIMILARITY.
FT	DISULFID	142	167	BY SIMILARITY.
FT	DISULFID	170	185	BY SIMILARITY.
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	435 AA;	46709 MW;	624626E6022F656F CRC64;
Query Match				
Best Local Similarity 6.6%; Score 228.5; DB 1; Length 435;				
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;				
QY	65	LTCDKCPAGTYVSEHCTNTSLRVCSSCPVCTFTRHENGIEKCHDCSOPC-PWPMIEKL-P	122	
DB	57	ICCSRCPPGYVSAKCSIRDTVCATCAENSYNEHWNLYLICQLC-RPCDPVMGLEBIAP	115	
QY	123	CAALTDRECHPCPGMFQSNATCAPHTV-----CPVGMGVRKKGTETE-----	164	
DB	116	CTSKRRTKQRCQPGMF-----CAWALECTHCELLSDCP-----PGTEALKDEVGKG	163	
QY	165	DVRKCKOCARCTESDVSSVMKCKAYTDCLSONLVWPKGTETDNVCGT---LPSFSS	220	
DB	164	NNHCVPCKAGHFONTSPSARCOPHTRCENQGLVEAAPGTAQSDTTCKNPLELPPEMSG	223	
QY	221	T 221		
DB	224	T 224		
RESULT 14				
TNRS5_BOVIN				
ID	TNR5_BOVIN	STANDARD;	PRT;	269 AA.
AC	Q28203;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 5 precursor			
DE	(CD40L receptor) (B-cell surface antigen CD40) (Fragment).			
GN	TNFRSF5 OR CD40.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
OC	Bovidae; Bovinae; Bos.			
NCBI_TaxID=9913;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97281252; PubMed=9135560;			
RA	Hirano A., Brown W.C., Estes D.M.;			
RT	"Cloning, expression and biological function of the bovine CD40			
RT	homologue; role in B-lymphocyte growth and differentiation in			
RT	cattle".			
RL	Immunology 90:294-300(1997).			
CC	-I- FUNCTION: Receptor for TNFSF5/CD40L.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
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OM protein - protein search, using sw model

Run on: July 11, 2003, 15:45:53 ; Search time 39 Seconds
(without alignments)

3460.535 Million cell updates/sec

Title: US-10-041-574-2

Perfect score: 3456

Sequence: 1 MGTSPPSSSTALASCSRIARR.....SQEASQTLLDSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2356	68.2	651	13 Q98SM6	Q98sm6 gallus gall
2	453	13.1	132	13 Q90Y18	Q90y18 salvelinus
3	354	10.2	83	13 Q8UWJ0	Q8uwj0 gallus gall
4	308	8.9	285	13 Q90W71	Q90w71 oncorhynch
5	307	8.9	285	13 Q90X56	Q90x56 oncorhynch
6	275.5	8.0	433	11 Q912M6	Q91zm6 rattus norv
7	275.5	8.0	459	11 Q623Z7	Q623z7 mus muscul
8	268.5	7.8	302	13 Q9PU50	Q9pus0 salvelinus
9	262.5	7.6	482	11 Q88734	Q88734 mus muscul
10	248.5	7.2	167	12 Q72762	Q72762 cowpox viru
11	248.5	7.2	167	12 Q8UYL3	Q8uyl3 vaccinia vi
12	240.5	7.0	167	12 Q9DJL2	Q9djl2 cowpox viru
13	238	6.9	351	12 Q57117	Q57117 cowpox viru
14	237.5	6.9	360	12 Q57118	Q57118 cowpox viru
15	233	6.7	351	12 Q57121	Q57121 cowpox viru
16	232.5	6.7	347	12 Q57119	Q57119 cowpox viru

17	231	6.7	277	6 Q8WMQ2	Q8wmq2 ovis aries
18	230.5	6.7	349	12 Q57100	Q57100 monkeypox v
19	230	6.7	348	12 Q57103	Q57103 monkeypox v
20	230	6.7	348	12 Q57108	Q57108 monkeypox v
21	230	6.7	348	12 Q57277	Q57277 monkeypox v
22	228.5	6.6	349	12 Q57102	Q57102 monkeypox v
23	228	6.6	347	12 Q57115	Q57115 cowpox viru
24	227.5	6.6	349	12 Q57101	Q57101 monkeypox v
25	227.5	6.6	349	12 Q57291	Q57291 monkeypox v
26	227	6.6	278	6 Q8SQ34	Q8sq34 sus scrofa
27	225.5	6.5	349	12 Q57099	Q57099 monkeypox v
28	225	6.5	355	12 Q85308	Q85308 cowpox viru
29	223.5	6.5	350	12 Q57116	Q57116 cowpox viru
30	221.5	6.4	349	12 Q57305	Q57305 cowpox viru
31	216.5	6.3	326	12 Q57120	Q57120 cowpox viru
32	215.5	6.2	351	12 Q73559	Q73559 cowpox viru
33	214.5	6.2	326	12 Q57122	Q57122 cowpox viru
34	212.5	6.1	350	12 Q57123	Q57123 cowpox viru
35	211.5	6.1	322	12 Q72761	Q72761 cowpox viru
36	208.5	6.0	349	12 Q57098	Q57098 camelpox vi
37	208.5	6.0	349	12 Q57109	Q57109 variola vir
38	208.5	6.0	349	12 Q8UYA7	Q8uya7 camelpox vi
39	208.5	6.0	349	12 Q57284	Q57284 camelpox vi
40	206.5	6.0	348	12 Q57112	Q57112 variola vir
41	206.5	6.0	348	12 Q85407	Q85407 variola vir
42	204.5	5.9	349	12 Q57110	Q57110 variola vir
43	204.5	5.9	349	12 Q57111	Q57111 variola vir
44	204.5	5.9	349	12 Q89098	Q89098 variola vir
45	204.5	5.9	349	12 Q89118	Q89118 variola vir

ALIGNMENTS

RESULT 1

Q98SM6 PRELIMINARY; PRT; 651 AA.
ID Q98SM6;
AC Q98SM6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.2; -.
DR HSSP; P19438; INCF.
DR InterPro; IPR003975; Shal_channel.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 68.2%; Score 2356; DB 13; Length 651;
Best Local Similarity 70.8%; Pred. No. 1.2e-181;
Matches 470; Conservative 47; Mismatches 101; Indels 46; Gaps 10;

QY 23 ATMTAGSLLLLGFLSTTTTAAQ-----EQKASNL-ICTYRHVRATGQVLTCKCPAGTVYS 77

Db 3 AAVLAAYLPLVLFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNOELICDKCPAGTYVS 62
QY 78 EHCINTSLRVCSSCPVCTFTRHENGIEKCHDCSQPCPWPMEKLPALCAALTDRECTCPGM 137
Db 63 KHKCTSLRCSGPCDGTFTKHENGIBRCHPCRPCELPMEIKHTCHTALDRECTCLSGT 122
QY 138 FQSNATCAPHTVCPVGVGVRKKGTEDETRCKOCARGTFSFSDVPSSVMKCKAYTDCLSONL 197
Db 123 FOINDTCVPVTVCPVGVGVRKKGTEDETRCKPCLRGTFSDVPSSVMKCKAYTDCLFCKNM 182
QY 198 VYKPGTKETDNCVG---TLP--SFSSSTSPSGTALFPPEHMEHEVPSSTVYVPGKM 252
Db 183 VYKPGTKESDNCVSPASLPNTSLTSSDAQDG-----ETVEAPPTAYLPKGLN 232
QY 253 STESNSASVPRKVLSSIQEGTVPDNTSSARGEDVKNLPLNQLVYVNHQGPGRHHLKL 312
Db 233 SVFDELSSPAPRVNGTAEPTVDYNDTSANGTVGAPGSLSSAGTAGOASVYRKHHTSQA 292
QY 313 L---PSMEATGGKSSPIKPKRGHPRQNLKHKHEDINEHLPWMLVFLLLVLVVIYVCS 369
Db 293 MGKQPAQEMAGGKSSIPYRPPRRGP--NVHQHEDINEHLPWMLVFLLLVLVVIYVCS 350
QY 370 IRKSSRTLKGPQDPSAIVEKAGLKKSWPTQNRKWIYVYCNHGHIDILKLVAAQVGSQ 429
Db 351 VRKSSRTLKGPQDPSAIVEKAIMKSTTPTQNRKWIYVYCNHGHIDILKLVAAQVGSQ 410
QY 430 WKDIYQFLCNASEREVAASNGYTADHERAYAAALQHWITRGPEASLAQLISALRQHRND 489
Db 411 WKDIYQFLCNASEREVAASNGYAADHERAYAAALQHWITRGPEASLAQLISALRQHRND 470
QY 490 VVEKIRGLMEDTT-----QLETKLALPMSPLSPSPSPNAKLE 531
Db 471 VVEKIRGLMEDTTPVQMOPQWQODCSNDGDKLEGDKLALPVSPSPSPVPTFSP--KPP 528
QY 532 NSALLTVPEPQDNKNGFFVDESEPLLRCDSTSGSSALSRSNGSPFITKEKKDVLQVRL 591
Db 529 DAAVLTVPEPSEK-KCFFVDESEPLLRCDSTSGSSALSRSNGSPFITKEKKDVLQVRL 587
QY 592 DPCDLOPFDMLHFNPELRIEIPQAEKDLRLFEIIGVKSEFASOTLLDSVYSHL 651
Db 588 DPCDLOPFDMLHILNPELHVEIPEIQAEDKDLRLFEIAGVKSQSEASOTLLDSVYSHL 647
QY 652 DLL 655
Db 648 DLL 651

RESULT 2

Q90Y18 PRELIMINARY; PRT; 132 AA.
AC Q90Y18;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Death receptor 6 (fragment).
GN DR6.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Boe J., Goetz F.W., Johnson A.L.;
RT "Conservation of Death Receptor-6 (DR6) in avian and piscine
vertebrates.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2001).
DR EMBL; AF302499; AAL09310.1; -;
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_2; 1.

KW Receptor.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 14303 MW; B01FED44260C1EB5 CRC64;
Query Match 13.1%; Score 453; DB 13; Length 132;
Best Local Similarity 56.1%; Pred. No. 6.3e-29;
Matches 74; Conservative 25; Mismatches 33; Indels 0; Gaps 0;
QY 74 TYVSEHCTNTSLRVCSSCPVCTFTRHENGIEKCHDCSQPCPWPMEKLPALCAALTDRECTC 133
Db 11 TFSVRHCTQNVNDCSCDEGTFTHGNGIHCRCRRPCRAPLVEKVPCTATSDRICTC 60
QY 134 PGMFQSNATCAPHTVCPVGVGVRKKGTEDETRCKOCARGTFSFSDVPSSVMKCKAYTDCL 193
Db 61 PPTFTQGDCTAHSCLCPVSGVYKRGNDVEDVRCACARGSFSDMASSVLRCKTHDCL 120
QY 194 SQNLVITKPGTK 205
Db 121 AQSILPILIAAGTR 132

RESULT 3

Q8UWJO PRELIMINARY; PRT; 83 AA.
AC Q8UWJO;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Death receptor 6 (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Shi Z., Onagbesan O.M., Williams J.;
RT "Apoptosis in chicken ovary";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432512; AAL35560.1; -;
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 83
SQ SEQUENCE 83 AA; 9506 MW; 28F8C880F655FADC CRC64;
Query Match 10.2%; Score 354; DB 13; Length 83;
Best Local Similarity 94.4%; Pred. No. 3.3e-21;
Matches 68; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 434 YQFLCNASEREVAASNGYTADHERAYAAALQHWITRGPEASLAQLISALRQHRNDVVEK 493
Db 1 YQFLCNASEREVAASNGYAADHERAYAAALQHWITRGPEASLAQLISALRQHRNDVVEK 60
QY 494 IRLGMDTTQLE 505
Db 61 IRLGMDTTTPVQ 72

RESULT 4

Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEAD KIDNEY;
 RA Pleguezuelos O., Secombes C.J.;
 RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RE EMBL: AJ315137; CA043329.1;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;
 Query Match 8.9%; Score 308; DB 13; Length 285;
 Best Local Similarity 35.6%; Pred. No. 9.7e-17;
 Matches 67; Conservative 22; Mismatches 79; Indels 20; Gaps 3;
 QY 53 TYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTTRHENGIEKCHDCSQP 112
 DB 30 TYIWRDDATGSLTCDLCAFGTYLLKHCTDKRSDCGPCPKSHYTIWNIYERQYCNRF 89
 QY 113 CPWPMEIKLPCAALTRECTCPGCMFOSNATCAPHTVCPVGWGVKRGKTETEDVRCQCA 172
 DB 90 CTADEIESVPTQLHNQCECKDGFYTHGSCSRHRCPPGEGVISNGTAHTDVKCEPCP 149
 QY 173 RGTFSVPSVMKCKAYTDCLSQNLVVIKPGTKETDNNVCGTLPFSFSSSTSPSPGTAIFPR 232
 DB 150 VGFFSAVSSSRKACQKESVCPGGTTI--PGNDMNDVYC-----SACTNGS----- 193
 QY 233 PEHNETHE 240
 DB 194 ----RTHE 197
 RESULT 5
 Q90Y56 PRELIMINARY; PRT; 285 AA.
 AC Q90Y56;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE TNF decoy receptor.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
 RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
 RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
 RT fragments containing AU-rich elements."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RE EMBL: AF401631; AA091758.1;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00181; EGF_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;
 Query Match 8.9%; Score 307; DB 13; Length 285;
 Best Local Similarity 38.4%; Pred. No. 1.2e-16;

Matches 61; Conservative 20; Mismatches 76; Indels 2; Gaps 1;
 QY 53 TYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTTRHENGIEKCHDCSQP 112
 DB 30 TYIWRDDATGSLTCDLCAFGTYLLKHCTDKRSDCGPCPKSHYTIWNIYERQYCNRF 89
 QY 113 CPWPMEIKLPCAALTRECTCPGCMFOSNATCAPHTVCPVGWGVKRGKTETEDVRCQCA 172
 DB 90 CTADEIESVPTQLHNQCECKDGFYTHGSCSRHRCPPGEGVISNGTAHTDVKCEPCP 149
 QY 173 RGTFSVPSVMKCKAYTDCLSQNLVVIKPGTKETDNNV 211
 DB 150 VGFFSAVSSSRKACQKESVCPGGTTI--PGNDMNDVYC 186
 RESULT 6
 Q912M6 PRELIMINARY; PRT; 433 AA.
 AC Q912M6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Tumor necrosis factor receptor type II (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
 RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
 RT capillary endothelial cells and participate in TNF-alpha transport
 RT through the blood-brain barrier."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RE EMBL: AF420214; AAL16021.1; -
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 3.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 433 433
 SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CAA CRC64;
 Query Match 8.0%; Score 275.5; DB 11; Length 433;
 Best Local Similarity 26.1%; Pred. No. 7.3e-14;
 Matches 83; Conservative 37; Mismatches 127; Indels 71; Gaps 11;
 QY 65 LTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFTTRHENGIEKCHDCSQPCPWPMEIKLPCA 124
 DB 33 MCCAACPPGQYAKHFCNKTSDTVCADCAAGNFTQVNNHLHTCLSCSSCSDDQVETHNCT 92
 QY 125 ALTDRECTCPGCMF-----OSNA--TCAPHIVCPVGWGVKRGKTETEDVRCQCA 177
 DB 93 KKQNRVACNADSYCALKLHSGNCRQCKMGKSCGPGFVARSRVTSNGNVCACAPGTF 152
 QY 178 DVPSVMKCKAYTDCLSQNLVVIKPGTKETDNNVCGTLPFSFSSSTSPS--PGTAIFPRPE- 234
 DB 153 DTTSTSDVCRPHRIC----SILAIPGNASTDAVCA-----SESPTSAVPTIYVQSEPE 203
 QY 235 ----HMETHPEVPSST--YVPKGMNST---ESNSASV----- 262
 DB 204 TRSQPMQDEPGSPQTPHIPVSLGSPITPEISITGIGSLPIGLVLTLLGLMLGLANCF 263
 QY 263 ----RPKVLSSIQEVTDPDNTSSARGKEDVKNKTLPLNQLVNVHQQPHRHILKLLPSMEA 318
 DB 264 ILVQRKKKPSCLQRETMVPHLPDEKSDAV-----GLEQQHLLTTAPSSSS 309
 QY 319 TGGEKSSPTPIKPKRGHP 336
 DB 310 SSLESSAS--AGDRRAP 325

RESULT 7

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Q62327 ID Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (Fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1CA4626DF CRC64;

Query Match 8.0%; Score 275.5; DB 11; Length 459;
Best Local Similarity 25.0%; Pred. No. 8e-14;
Matches 82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;

QY 65 LTCDCPCAGTGVSEHCNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMPMIEKLPCA 124
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 38 MCCACPPGGQYVHFNCNKTSDTVCADEASMYTQVWQNFRTCLSCSSCSTDOVETRACT 97
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 125 ALTDRECTCPGPFQSNAT-----CAPHTVCPGVGWVKKKTETEDVRCKCARGTFS 177
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 98 KOONRYCACEAGRYCALKTHSGSCRCQMRSLKCGPGFVASSRAPNGVNLCKACAPGTFS 157
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 DVPSSVKKKAYDCLSONLVKPGTKETDNVCGTLPLSPSSSTSPGTAIPRPHEME 237
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 158 DTSSSDVCRPHRIC-----SILAIPGNASTDAVCA-----PESPT 193
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 THEVPSTVY-----PKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVKNKLP 293
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 LSAIPRTLVSQPEPRSRQPLDQEPGSPQTPSLTSL--GSTPIIQSTKG-----GISLP 247
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 294 -----NLQVNV-----HQQGFH-----HRIILK 311
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 248 IGLIVGVTSLGLMLGLVNCFLVLRKKPKSLQORDAKVPHVPDEKSDQAVGLEQOHLIT 307
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 312 LLPSMEATGGEKSS--PIKPKRKHPR 337
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 TAPSSSSSLESASAGDRAPPGGHQ 335
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 8

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Q9PUS0 ID Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation.";
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSP; O14763; ID4V.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 7.8%; Score 268.5; DB 13; Length 302;
Best Local Similarity 32.5%; Pred. No. 1.6e-13;
Matches 53; Conservative 26; Mismatches 81; Indels 3; Gaps 2;

QY 53 TYRHVDRTGVLTCDCPCAGTGVSEHCNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQP 112
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 22 TFKNDRRYSGLSIVCDRCPPGYLRAPCSAMRKSDEACPNAGYTFEWNHISKLCRCSM- 80
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 113 CPWPMIEKLPCAALTDRECTCPGPFQSNATCAPHTVCPGVGWVKKKTETEDVRCKQ 170
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 81 CAENQVQVQECSPSNNCECECKEGYVFNKKYEACIKHKECPGPGYANTTGTPHQDTECVQ 140
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 171 CARGTSDVPSSVKKKAYDCLSONLVKPGTKETDNVCGT 213
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 141 CQAGFYSESSAKATCAOSNCKVGLRVVYKGDWHHTLCAS 183
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
Q88734 ID Q88734 PRELIMINARY; PRT; 482 AA.
AC Q88734;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P80 TNF-alpha receptor.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98414512; PubMed=9740674;
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT and Characterization of the two Transcripts.";
RL Genomics 52:79-98(1998).
DR EMBL; Y14619; CAA74969.1; -.

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DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 7.6%; Score 262.5; DB 11; Length 482;
Best Local Similarity 24.4%; Pred. No. 9.6e-13;
Matches 82; Conservative 33; Mismatches 128; Indels 93; Gaps 11;

QY 65 LTCDCPAGYVSEHCNT-----SLRVSSCPVGTFTTRHENGIEKCHDCSQPCWPM 117
   : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 MCCAKCPGQYVKHFCNKTSDTVCADSDTVCADCEASMYQVWNQFRTCLSCSSCSTDQ 112

QY 118 IEKLPAAALTDRECTPPGQFNAT-----CAPHTVCPVGVGVRKKGTTETEDVRCKQ 170
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 VETRACTKQONRYCACEAGRYCALKTHSGSCRCQMLSKCGPGFGVASSRAPNGVLCKA 172

QY 171 CARGTSDVPSSVMKCKAYTDCLSQNLVWIKPGTKETDNVCGTLPFSFSSSTSPGTAIF 230
   || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 173 CARGTSDTSSDVCPRHIC-----SILAIGNASTDAVCA----- 210

QY 231 PRPEHMETHEVPSTVY----PKGMNSTESNSASVRPKVLSIIQEGTVPDNTSSARGKE 286
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 211 --PESPTLSAIPRLTYVSQPEPTRSQPLDQEPGSPQPSILTSL--GSTPIIEQSTKG-- 264

QY 287 DVNKLTP-----NLQVNV-----HQQGPH----- 305
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 265 --GISLPGLIVGTSIGLMLGLVNCFILVQRKKPKSCLOQDAKVPHVDPDEKSDQAVGL 322

QY 306 -HRHILKLLPSMEATGKESSTPT---KGPKRGHPR 337
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 323 EQQHLLTAPSSSSSSLESSASAGDRRAPGGHPQ 358

RESULT 10
O72762 PRELIMINARY; PRT; 167 AA.
AC O72762;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE K3R protein.
GN K3R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90.
RA MEDLINE=9829462; PubMed=9568042;
RA Stchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox, and vaccinia viruses."
RL Virology 243:432-460(1998).
DR EMBL; Y15035; CAA75301.1; -.
DR HSP; P19438; IEXT.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 167 AA; 18526 MW; 3B4A0D5A67F73961 CRC64;
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Query Match 7.2%; Score 248.5; DB 12; Length 167;
Best Local Similarity 34.7%; Pred. No. 2.9e-12;
Matches 59; Conservative 16; Mismatches 78; Indels 17; Gaps 5;

QY 30 LLLIGFLSTTTAQPEOKASNLIGTYRHVDRTATGQVLTCDK-CPAGTYVSEHCNTSLRVC 88
   : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 IILIGFLIINTSLSMKCEQGVSY-----NSQELKCKCKLGLGTYSDHRCDKYSTIC 58

QY 89 SSCPVGTFTTRHENGIEKCHDCSQPCWPWMIKLPAAALTDRECTPPGMF-----QSN 141
   || ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 GHCPSTFTTSIYNRSPWCHSCRGPGCTNRVEVTPCTPTTNRICHCDNSYCLLKASDGN 118

QY 142 ATCAPHTVCPVGVGVRKKG--TETEDVRCKOCARGTSDVPSSVMKCKAYT 190
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 VTCAPKTKCGRGYG--KKGEDEMGNTICKCKRGTYSDIVSDSDQCKPMT 166

RESULT 11
Q8UYL3 PRELIMINARY; PRT; 167 AA.
AC Q8UYL3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CrME protein.
GN CrME.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USSR.
RA Reading P.C., Khanna A., Smith G.L.;
RT "Vaccinia virus CrME encodes a soluble and cell-surface tumor necrosis
RT factor receptor that contributes to virus virulence."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315962; CAC83048.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 167 AA; 18510 MW; 3B4A0D4A27B797D CRC64;

Query Match 7.2%; Score 248.5; DB 12; Length 167;
Best Local Similarity 34.7%; Pred. No. 2.9e-12;
Matches 59; Conservative 16; Mismatches 78; Indels 17; Gaps 5;

QY 30 LLLIGFLSTTTAQPEOKASNLIGTYRHVDRTATGQVLTCDK-CPAGTYVSEHCNTSLRVC 88
   : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 IILIGFLIINTSLSMKCEQGVSY-----NSQELKCKCKLGLGTYSDHRCDKYSTIC 58

QY 89 SSCPVGTFTTRHENGIEKCHDCSQPCWPWMIKLPAAALTDRECTPPGMF-----QSN 141
   || ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 GHCPSTFTTSIYNRSPWCHSCRGPGCTNRVEVTPCTPTTNRICHCDNSYCLLKASDGN 118

QY 142 ATCAPHTVCPVGVGVRKKG--TETEDVRCKOCARGTSDVPSSVMKCKAYT 190
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 VTCAPKTKCGRGYG--KKGEDEMGNTICKCKRGTYSDIVSDSDQCKPMT 166

RESULT 12
Q9DJL2 PRELIMINARY; PRT; 167 AA.
AC Q9DJL2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CrME protein.
GN CrME.
OS Cowpox virus (CPV).
```

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OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ELEPHANTPOX;
RX MEDLINE=20569353; PubMed=11119592;
RA Saraiva M., Alcamí A.;
RT "CrME, a novel soluble tumour necrosis factor receptor encoded by
RT Poxviruses";
RL J. Virol. 75:226-233(2001).
DR EMBL: AJ272008; CAC15562.1; -.
DR HSSP: P19438; 1EXT.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 167 AA; 18500 MW; FB790E7927F91680 CRC64;

Query Match 7.0%; Score 240.5; DB 12; Length 167;
Best Local Similarity 34.1%; Pred. No. 1.3e-11;
Matches 58; Conservative 16; Mismatches 79; Indels 17; Gaps 5;

QY 30 LLLGLFLSTTTAQQEOKASNLIGTYRHVDRATGQVLTCDK-CPAGTYVSEHCTNTSLRVC 88
DB 5 IIIIGFLIINTSLSMKCEQGSYY-----NSQELKCKCKLKPGRYSDHRCDKYSDDTC 58
QY 89 SSCPVGTFTFRHENGIEKCHDCSQCPWPWMIKLPKCAALTDRECTCPGPMF-----QSN 141
DB 59 GHCPSTFTSIYRSPWCHSCRGSCGTNRVEVTPCTPTTNRIHCHDCNSYCLLKASDGNC 118
QY 142 ATCAPHTVCPVGMGVRKKG-TETEDVRCKOCARGTESDVPSSVMKCKAVT 190
DB 119 VTCAPTKCGRGY--KKGEDEMGNTICKCKRGTYSDIVSDQCKPMT 166

RESULT 13
O57117
ID O57117 PRELIMINARY; PRT; 351 AA.
AC O57117;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUNICH OPV 85(HUMAN);
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT "Detection and differentiation of old world orthopoxviruses:
RT restriction fragment length polymorphism of the crmb gene region.";
RL J. Clin. Microbiol. 39:94-100(2001).
DR EMBL: U90227; AA894383.1; -.
DR HSSP: O14763; IDOG.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 351 AA; 38304 MW; 57C84FFEF5B5F57E CRC64;

Query Match 6.9%; Score 238; DB 12; Length 351;
Best Local Similarity 26.1%; Pred. No. 5.8e-11;
Matches 83; Conservative 27; Mismatches 116; Indels 92; Gaps 12;

QY 65 LTCDKCAPAGTYVSEHC---TNTSLRVCSCPVGTFTRHENGIEKCHDCSQCPWPWMIK 121
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DB 42 LCCLSCPPGTYSRLCDSKTNTNTQ-CTPCGSGTFTSHNHLPACLSCNGRCDNSQVETR 100
QY 122 PCAALTDRECTCPGPMF-----QSNATCAPHTVCPVGMGVRKKGTTETEDVRCKQCARGT 175
DB 101 PCNTTHNRICECSPGYCYLLKGGSSGCKACVSQTKCGYGV-SGHTSTGDVICSPCLGT 159
QY 176 FSDVPSSVMKCKAY-----TDC-----LSQNL----- 197
DB 160 YSHTVSSADKCEVPSPNTFNIDVEINLYPVNDTSTRTTTTGLSESISTSELTITMNHK 219
QY 198 -----VVIKPGT-----KETDNV-----CGTLPFSSTSPSPGT 227
DB 220 DCDPVPFRDGYFVLNKAATSGEFTGENRYQNTSNVCTLNFELKCNKNDSSSKQLTKTKND 279
QY 228 AIFPRPEHMETHEVPSSTVYPKGMNSTE-----SNSASVRPKVLSSIOEGTVPDNTSSA 282
DB 280 TIMP-----HSET-----VTLVGDCLSVDIYIILYSNTQDYETDTTISYHAGNLYYVDSHM 331
QY 283 RGEDVNVKTLPLNLQVNVH 300
DB 332 PGSCDIHKLITNSQNPTH 349

RESULT 14
O57118
ID O57118 PRELIMINARY; PRT; 360 AA.
AC O57118;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CPV58;
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT "Detection and differentiation of old world orthopoxviruses:
RT restriction fragment length polymorphism of the crmb gene region.";
RL J. Clin. Microbiol. 39:94-100(2001).
DR EMBL: U90229; AA894385.1; -.
DR HSSP: O14763; IDOG.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 360 AA; 39370 MW; 3628AD87E4709378 CRC64;

Query Match 6.9%; Score 237.5; DB 12; Length 360;
Best Local Similarity 24.7%; Pred. No. 6.6e-11;
Matches 88; Conservative 31; Mismatches 136; Indels 101; Gaps 12;

QY 30 LLLGLFLSTTTAQQEOKASN---LIGTYRHVDRATGQVLTCDKCAPAGTYVSEHC---TWT 83
DB 7 LLLLSCTIIINSETPHEPSNGKCKDNEYKH-----HLLCCLSCPPGTYSRLCDSKTWT 60
QY 84 SLRVCSQCPVGTFTRHENGIEKCHDCSQCPWPWMIKLPKCAALTDRECTCPGPMF----- 138
DB 61 NTQ-CTSCGSGTFTSRNNHLPACLSCNGRCDNSQVETRSCNTTHNRICSPGYCYLLKG 119
QY 139 -QSNATCAPHTVCPVGMGVRKKGTTETEDVRCKQCARGTESDVPSSVMKCKAY----- 189
DB 120 SSGCRACVSQTKCGMGYGV-SGHTPTGDIVICSPCGLGTYSHTVSSADKCEPVPNTFVI 178
QY 190 -----TDC-----LSQNLVVIKPGTKETDNV----- 210
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Db 179 DVEINLYPVNDTSCRTTTTGLSEISTSELIITMNHKDDPVRDGYFVSLNKVATSGF 238
QY 211 -----CGTLPSFSSTSPSPTAIFPRPEHMETHEVPSSYVVK 249
Db 239 FTGENYQNLKSVCTLNFEIKCNKDKSSSKQLTKAKNDTNP---HSET-----VTLVGD 290
QY 250 GNMSTE-----SNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVKNKTLPLNLQVNH 300
Db 291 CLSSVDIILYSNTQDYEITISYHAGNVLDVDSHMPGSCDIHKLITNSQNP 346
CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_taxid=10243;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-MUNICH Opv89/4 (CAT);
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT detection and differentiation of old world orthopoxviruses;
RL J. Clin. Microbiol. 39:94-100(2001).
DR EMBL; U90232; AAB94388.1;
DR HSSP; O14763; 1DOG.
DR InterPro; IPR001388; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
KW PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
KW Receptor.
SQ SEQUENCE 351 AA; 38394 MW; 6D0E4040C0E0EF78 CRC64;
```

RESULT 15

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057121
ID O57121 PRELIMINARY; PRT; 351 AA.
AC O57121;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_taxid=10243;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-MUNICH Opv89/4 (CAT);
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT detection and differentiation of old world orthopoxviruses;
RL J. Clin. Microbiol. 39:94-100(2001).
DR EMBL; U90232; AAB94388.1;
DR HSSP; O14763; 1DOG.
DR InterPro; IPR001388; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
KW PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
KW Receptor.
SQ SEQUENCE 351 AA; 38394 MW; 6D0E4040C0E0EF78 CRC64;

Query Match
Best Local Similarity 24.9%; Score 233; DB 12; Length 351;
Matches 82; Conservative 27; Mismatches 122; Indels 98; Gaps 11;

QY 54 YRHVDRATGQVLTCDKCPAGTYVSEHC---TNTSLRVCSGPCVGTTRHENGIEKCHDCS 110
Db 37 YKH-----HHLGCLSCPPTGYASRLCDSKTNTNQ-CTSCGSGTFTSRNNHLPACLSCN 89
QY 111 QPCPWPMEIKLPAAALTDRECTPPGMF-----QSNATCAPHTVCPVGWGVKKGKETE 164
Db 90 GRCDNQVETRSNTTHNRICECPGYCYLLKGSSGCKACVQTKCGMGYGV-SGHTSTG 148
QY 165 DVRCQCARGTFSVPSSVMKCKAY-----TDC-----LS 194
Db 149 DVICSPCGLGTYSHTVSSADKCEPVPNTFNIDVEINLYPVNDTSCRTTATGLSEIS 208
QY 195 QNLVVIKPGTKEIDNV-----CGTLPS 216
Db 209 TSELTITMNHKDDPVRDGYFVSLNKVATSGFTGENRYQNTSKVCTLNFEIKCNKDS 268
QY 217 FSSSTSPSPTAIFPRPEHMETHEVPSSYVVKGMNSTE-----SNSSASVRPKVLSSIQ 271
Db 269 SSQQLTKNDTNP---HSET-----VTLVGDCLSSVDIILYSNTQDYEITISYH 320
QY 272 EGTVPDNTSSARGKEDVKNKTLPLNLQVNH 300
Db 321 AGNVLDVDSHMPGSCDIHKLITNSQNP 349
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Search completed: July 11, 2003, 15:48:27
Job time : 41 secs

